

10-791-592

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2005, 11:27:37 ; Search time 154 Seconds  
(without alignments)  
871.200 Million cell updates/sec

Title: US-10-791-592-2  
Perfect score: 1970  
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		8						
Result	No.	Score	Query		DB	ID	Description	
			Match	Length				
1	1970	100.0	374	2	AAR79165	Aar79165	Human	mon
2	1970	100.0	374	4	AAG80107	Aag80107	Human	CCR
3	1970	100.0	374	6	ABU09083	Abu09083	Human	che
4	1970	100.0	374	7	ADD44861	Add44861	Human	Pro
5	1970	100.0	374	7	ADD44865	Add44865	Human	Pro
6	1970	100.0	374	7	ADP65146	Adp65146	Human	che
7	1970	100.0	374	8	ADO29221	Ado29221	Human	GPC
8	1823	92.5	344	5	ABG92881	Abg92881	Class I	r
9	1823	92.5	344	6	ABU61655	Abu61655	Human	mon

10	1823	92.5	344	7	ADF72129	Adf72129	Human	G-p
11	1823	92.5	344	8	ADP86217	Adp86217	Human	MCP
12	1727.5	87.7	329	4	AAB46859	Aab46859	Human	MCP
13	1727.5	87.7	329	5	ABB81055	Abb81055	Human	MCP
14	1651.5	83.8	360	2	AAR79166	Aar79166	Human	mon
15	1651.5	83.8	360	2	AAW35833	Aaw35833	Human	mon
16	1651.5	83.8	360	4	AAG80108	Aag80108	Human	CCR
17	1651.5	83.8	360	4	AAU07614	Aau07614	Human	wil
18	1651.5	83.8	360	6	ABP97725	Abp97725	Amino	aci
19	1651.5	83.8	360	6	ABP81987	Abp81987	Human	C-C
20	1651.5	83.8	360	8	ADM67225	Adm67225	Human	adi
21	1651.5	83.8	360	8	ADL82831	Adl82831	Human	PRO
22	1650.5	83.8	360	4	AAU07613	Aau07613	Human	CCR
23	1645.5	83.5	360	4	ABB56340	Abb56340	Non-endog	
24	1589.5	80.7	347	7	ADF56627	Adf56627	Partial	h
25	1332.5	67.6	373	8	ADM67224	Adm67224	Murine	ad
26	1332.5	67.6	373	8	ADO29222	Ado29222	Mouse	GPC
27	1332.5	67.6	373	8	ADP74040	Adp74040	Murine	CC
28	1244	63.1	354	8	ADO29228	Ado29228	Mouse	GPC
29	1236	62.7	352	4	AAG79089	Aag79089	Amino	aci
30	1234	62.6	354	2	AAW54037	Aaw54037	Mouse	CC-
31	1230	62.4	354	7	ADD44859	Add44859	Rat	Prote
32	1230	62.4	354	7	ADD44863	Add44863	Rat	Prote
33	1224	62.1	352	2	AAW27407	Aaw27407	Human	CCR
34	1224	62.1	352	2	AAW27123	Aaw27123	Human	che
35	1224	62.1	352	2	AAW27125	Aaw27125	Macaque	c
36	1224	62.1	352	2	AAW23835	Aaw23835	Human	CC
37	1224	62.1	352	2	AAW88232	Aaw88232	HIV-1	co-
38	1224	62.1	352	4	AAE07048	Aae07048	Human	G-p
39	1224	62.1	352	4	AAG80111	Aag80111	Human	CCR
40	1224	62.1	352	4	AAE04321	Aae04321	Human	che
41	1224	62.1	352	4	AAE07039	Aae07039	Human	G-p
42	1224	62.1	352	4	AAB46858	Aab46858	Human	HDG
43	1224	62.1	352	4	AAB83354	Aab83354	Human	CCR
44	1224	62.1	352	4	AAB82948	Aab82948	Human	HIV
45	1224	62.1	352	5	AAU97152	Aau97152	Human	G-p

# ALIGNMENTS

## RESULT 1

AAR79165

ID AAR79165 standard; protein; 374 AA.

XX

AC AAR79165;

XX

DT 25-MAR-2003 (revised)

DT 29-DEC-1995 (first entry)

XX

DE Human monocyte chemoattractant protein-1 receptor MCP-1RA.

XX

KW Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1. .48  
 FT /label= extracellular  
 FT Domain 49. .70  
 FT /label= transmembrane  
 FT Domain 80. .700  
 FT /label= transmembrane  
 FT Domain 115. .136  
 FT /label= transmembrane  
 FT Domain 154. .178  
 FT /label= transmembrane  
 FT Domain 204. .231  
 FT /label= transmembrane  
 FT Domain 244. .268  
 FT /label= transmembrane  
 FT Domain 295. .313  
 FT /label= transmembrane  
 FT Region 314. .375  
 FT /label= carboxyl tail

XX

PN W09519436-A1.

XX

PD 20-JUL-1995.

XX

PF 11-JAN-1995; 95WO-US000476.

XX

PR 13-JAN-1994; 94US-00182962.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Charo I, Coughlin S;

XX

DR WPI; 1995-263866/34.

DR

N-PSDB; AAQ96297.

XX

PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.  
 PT for identifying antagonists and for treating diseases characterised by  
 PT monocytic infiltrates.

XX

PS Claim 2; Fig 1; 84pp; English.

XX

CC To identify and clone new members of the chemokine receptor gene family,  
 CC degenerate oligo primers were designed corresp. to the conserved  
 CC sequences R79167 in the second and R79168 in the third transmembrane  
 CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the  
 CC HUMSTRS orphan receptor (GenBank Accession #M99293. The degenerate oligo  
 CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and  
 CC Q96300. Amplification of cDNA derived from MM6 cells with the primers  
 CC yielded a number of PCR products. One cDNA appeared to encode a novel  
 CC protein. To obtain a full-length version of this clone, a MM6 cDNA  
 CC library was constructed in pFROG and probed with the PCR product. A 2.1  
 CC kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA  
 CC library revealed a second sequence that was identical to the 2.1 kb cDNA  
 CC sequence first obtd. from the 5' UTR through the putative seventh  
 CC transmembrane domain but contained a different cytoplasmic tail. The  
 CC second sequence appears to represent alternative splicing of the carboxyl  
 CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-  
 CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-

CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.  
CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN  
CC field.)

XX

SQ Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 2; Length 374;  
Best Local Similarity 100.0%; Pred. No. 4.9e-215;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
          ||||||||||||
Db    361 GRAPEASLQDKEGA 374
```

## RESULT 2

AAG80107

ID AAG80107 standard; protein; 374 AA.

XX

AC AAG80107;

XX

DT 17-JAN-2002 (first entry)

XX

DE Human CCR2a protein.

XX

KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;  
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;  
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;  
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;  
KW antirheumatic; antiarthritic.

XX

OS Homo sapiens.

XX





```

      |||
Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
Qy      241 AVRVI FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
      |||
Db      241 AVRVI FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
Qy      301 NP IIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
      |||
Db      301 NP IIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
Qy      361 GRAPEASLQDKEGA 374
      |||
Db      361 GRAPEASLQDKEGA 374

```

RESULT 3

ABU09083

ID ABU09083 standard; protein; 374 AA.

XX

AC ABU09083;

XX

DT 23-JUL-2003 (first entry)

XX

DE Human chemokine receptor-2 (CKR-2) polypeptide.

XX

KW Human; thymus expressed chemokine; TECK; chemokine; MIP-3alpha; receptor;

KW MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma;

KW monocyte/dendritic cell receptor for chemokine; inflammatory condition;

KW abnormal physiology; abnormal proliferation; degeneration; atrophy;

KW antiinflammatory; antiasthmatic; cytostatic; chemokine receptor-2; CKR-2.

XX

OS Homo sapiens.

XX

PN US2003018167-A1.

XX

PD 23-JAN-2003.

XX

PF 03-JAN-2002; 2002US-00039659.

XX

PR 05-JUL-1996; 96US-0021664P.

PR 11-OCT-1996; 96US-0028329P.

PR 04-JUN-1997; 97US-0048593P.

PR 03-JUL-1997; 97US-00887977.

XX

PA (SCHE ) SCHERING CORP.

XX

PI Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;

XX

DR WPI; 2003-416900/39.

XX

PT New chemokines, TECK, MIP-3 alpha, MIP-3 beta, DC CR and M/DCCR, useful

PT for treating conditions associated with abnormal physiology or

PT development, including inflammatory conditions (e.g. asthma), and

PT abnormal proliferation.

XX

PS Disclosure; Page 9-10; 54pp; English.

XX  
 CC The invention relates to nucleic acids encoding the chemokines TECK, MIP-  
 CC 3alpha, MIP-3beta, DC CR and M/DC CR. The polypeptide sequences are  
 CC useful in isolating DNA clones encoding the chemokines, for generating  
 CC antibodies, and for predicting oligonucleotides for screening a library  
 CC to isolate species variants. A nucleic acid encoding a chemokine  
 CC polypeptide can be used to identify genes, mRNA and cDNA species which  
 CC encode related or homologous ligands, as well as DNA encoding homologous  
 CC proteins from different species. The chemokines and antibodies which bind  
 CC to the polypeptides are useful in the treatment of conditions associated  
 CC with abnormal physiology or development, including inflammatory  
 CC conditions such as asthma, abnormal proliferation, regeneration,  
 CC degeneration and atrophy. This sequence represents the human chemokine  
 CC receptor-2 (CKR-2) polypeptide, used in the scope of the invention  
 XX  
 SQ Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 6; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-215;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
Db	301	NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
Qy	361	GRAPEASLQDKEGA	374
Db	361	GRAPEASLQDKEGA	374

RESULT 4  
 ADD44861  
 ID ADD44861 standard; protein; 374 AA.  
 XX  
 AC ADD44861;  
 XX  
 DT 29-JAN-2004 (first entry)

XX  
 DE Human Protein P41597, SEQ ID NO 10292.  
 XX  
 KW Human; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003016475-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 14-AUG-2002; 2002WO-US025765.  
 XX  
 PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX  
 PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX  
 DR WPI; 2003-268312/26.  
 DR GENBANK; P41597.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 PS Claim 1; Page; 1017pp; English.  
 XX  
 CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 7; Length 374;  
Best Local Similarity 100.0%; Pred. No. 4.9e-215;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
          ||||||||||||
Db    361 GRAPEASLQDKEGA 374
```

RESULT 5

ADD44865

ID ADD44865 standard; protein; 374 AA.

XX

AC ADD44865;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human Protein P41597, SEQ ID NO 10296.

XX

KW Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

XX

OS Homo sapiens.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.



Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
Db	301	NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
Qy	361	GRAPEASLQDKEGA	374
Db	361	GRAPEASLQDKEGA	374

RESULT 6

ADP65146

ID ADP65146 standard; protein; 374 AA.

XX

AC ADP65146;

XX

DT 12-AUG-2004 (first entry)

XX

DE Human chemokine (C-C motif) receptor 2, isoform A, chemokine (C-C).

XX

KW autoimmune disease; arthritide; gene expression analysis;

KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;

KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;

KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;

KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;

KW immune; human.

XX

OS Homo sapiens.

XX

PN WO2003072827-A1.

XX

PD 04-SEP-2003.

XX

PF 31-OCT-2002; 2002WO-US035433.

XX

PR 31-OCT-2001; 2001US-0336220P.

XX

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX

PI Hirsch R, Thorton SL;

XX





Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240  
 Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300  
 Qy 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360  
 Qy 361 GRAPEASLQDKEGA 374  
 |||||||||||||  
 Db 361 GRAPEASLQDKEGA 374

RESULT 7

ADO29221

ID ADO29221 standard; protein; 374 AA.

XX

AC ADO29221;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human GPCR CCR2, SEQ ID NO:322.

XX

KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 KW transgenic mouse; neurological disorder; adrenal gland disorder;  
 KW colon disorder; intestinal disorder; cardiovascular disorder;  
 KW muscular disorder; blood disorder; immune disorder; bone disorder;  
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
 KW kidney disorder; liver disorder; lung disorder; breast disorder;  
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
 KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
 KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
 KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
 KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;  
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
 KW receptor.

XX

OS Homo sapiens.

XX

PN WO2004040000-A2.

XX

PD 13-MAY-2004.

XX

PF 09-SEP-2003; 2003WO-US028226.

XX

PR 09-SEP-2002; 2002US-0409303P.

PR 09-APR-2003; 2003US-0461329P.

XX

PA (PRIM-) PRIMAL INC.

XX

PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX

DR WPI; 2004-390329/36.

DR N-PSDB; ADO29829.

XX

PT Novel mammalian G protein coupled receptors, useful for identifying  
PT compounds that modulates diagnosing and treating disease condition  
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
PT pectoris, Parkinson's disease.

XX

PS Claim 151; SEQ ID NO 322; 542pp; English.

XX

CC The invention relates to human and mouse G protein-coupled receptors  
CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
CC of the invention; methods of treating, preventing or diagnosing diseases  
CC associated with GPCRs of the invention; methods of screening for  
CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
CC from the transgenic mice; kits comprising several mice, each of which has  
CC a mutation in a different GPCR gene of the invention; and kits comprising  
CC probes which hybridise to GPCR polynucleotides of the invention. The  
CC invention further discloses variants of the GPCR polypeptides and vectors  
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
CC be used in the diagnosis, treatment or prevention of a wide variety of  
CC diseases including neurological disorders (e.g., Alzheimer's disease,  
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
CC disorders of the adrenal gland; disorders of the colon or intestine  
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the  
CC invention. Note: The full sequence data for this patent did not form part  
CC of the printed specification; those sequences not shown were obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX

SQ Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 8; Length 374;

Best Local Similarity 100.0%; Pred. No. 4.9e-215;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60  
  
Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFEGNAMCKLFTGLY 120  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFEGNAMCKLFTGLY 120  
  
Qy 121 HIGYFGGIIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Db	121	 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
Db	301	 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
Qy	361	GRAPEASLQDKEGA	374
Db	361	 GRAPEASLQDKEGA	374

RESULT 8

ABG92881

ID ABG92881 standard; peptide; 344 AA.

XX

AC ABG92881;

XX

DT 19-NOV-2002 (first entry)

XX

DE Class I receptors WSXWS motif.

XX

KW Immunoglobulin; variable heavy chain; variable light chain; human;

KW G-protein chemokine receptor; CCR5; HDGMR10; cancer; inflammation;

KW immunologic deficiency syndrome; blood protein disorder; nephritis;

KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;

KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;

KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;

KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;

KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;

KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;

KW lymphocytopenia.

XX

OS Synthetic.

XX

PN WO200264612-A2.

XX

PD 22-AUG-2002.

XX

PF 08-FEB-2002; 2002WO-US003634.

XX

PR 09-FEB-2001; 2001US-00779880.

PR 09-FEB-2001; 2001WO-US004153.

PR 12-JUN-2001; 2001US-0297257P.

PR 08-AUG-2001; 2001US-0310458P.

PR 12-OCT-2001; 2001US-0328447P.

PR 21-DEC-2001; 2001US-0341725P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX  
 PI Roschke V, Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2002-643455/69.  
 XX  
 PT New human G-protein Chemokine Receptor gene (HDGNR10) useful for  
 PT treating, preventing, ameliorating or monitoring diseases or disorders  
 PT associated with aberrant expression of HDGNR10 e.g. cancer.  
 XX  
 PS Example 17; Page 386; 562pp; English.  
 XX  
 CC The invention describes an isolated polynucleotide encoding a first  
 CC antibody at least 95-100% identical to a second antibody consisting of an  
 CC amino acid sequence comprising at least one, two or three CDR regions of  
 CC a variable heavy (VH) or variable light (VL) domain of the antibody  
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,  
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,  
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody  
 CC is useful treating, preventing, ameliorating, prognosing or monitoring  
 CC cancers or other diseases or disorders e.g. immunologic deficiency  
 CC syndromes such as blood protein disorders and ataxia telangiectasia,  
 CC inflammation associated disorders such as endotoxin lethality, nephritis  
 CC and inflammatory bowel disease, conditions associated with an increase in  
 CC certain haematopoietic cells such as histiocytosis, defective or aberrant  
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,  
 CC an infectious disease, an autoimmune disease such as Addison's disease,  
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative  
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or  
 CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,  
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a  
 CC disease or disorder associated with aberrant expression of novel human G-  
 CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid  
 CC sequence of the WSXWS motif found in class I receptors  
 XX  
 SQ Sequence 344 AA;

Query Match 92.5%; Score 1823; DB 5; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-198;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60  
 Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120  
 Qy 138 RYLAIVHAVFALKARTVTFGVVT SVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFPRG 197  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 RYLAIVHAVFALKARTVTFGVVT SVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFPRG 180  
 Qy 198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240  
 Qy 258 PYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317

```

                |||
Db      241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300
QY      318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
                |||
Db      301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344

```

RESULT 9

ABU61655

ID ABU61655 standard; protein; 344 AA.

XX

AC ABU61655;

XX

DT 08-AUG-2003 (first entry)

XX

DE Human monocyte chemoattractant protein 1 (MCP-1) receptor.

XX

KW Human; G-protein chemokine receptor; receptor; HDGNR10; MCP-1;

KW 7-transmembrane receptor; monocyte chemoattractant protein 1.

XX

OS Homo sapiens.

XX

PN US2003023044-A1.

XX

PD 30-JAN-2003.

XX

PF 03-SEP-2002; 2002US-00232686.

XX

PR 06-JUN-1995; 95US-00466343.

PR 18-NOV-1998; 98US-00195662.

PR 25-JUN-1999; 99US-00339912.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Li Y, Ruben SM;

XX

DR WPI; 2003-456307/43.

XX

PT Producing an antibody, involves immunizing an animal with a polypeptide

PT or with a polypeptide encoded by the human G-protein chemokine receptor

PT clone in ATCC 97183, and recovering the antibody.

XX

PS Disclosure; Fig 2; 23pp; English.

XX

CC The invention relates to a method of producing an antibody, involving

CC immunising an animal with a human G-protein chemokine receptor (HDGNR10)

CC polypeptide (also referred to as a human 7-transmembrane receptor) and

CC recovering an antibody which binds the polypeptide. The method is useful

CC for producing an antibody which binds specifically to the human G-protein

CC chemokine receptor polypeptide. This sequence represents the monocyte

CC chemoattractant protein 1 (MCP-1) receptor which shares homology with the

CC HDGNR10 polypeptide of the invention

XX

SQ Sequence 344 AA;

Query Match

92.5%; Score 1823; DB 6; Length 344;

Best Local Similarity 100.0%; Pred. No. 2.4e-198;  
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
          |||
Db      1  EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy      78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
          |||
Db      61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy     138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
          |||
Db     121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy     198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
          |||
Db     181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240

Qy     258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
          |||
Db     241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300

Qy     318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
          |||
Db     301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344
```

RESULT 10

ADF72129

ID ADF72129 standard; protein; 344 AA.

XX

AC ADF72129;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human G-protein chemokine receptor (CCR5) ligand MCP-1.

XX

KW cytostatic; CCR5 modulator; antibody; G-protein chemokine receptor; CCR5;

KW cancer detection; cancer diagnosis; cancer prognosis; cancer monitoring;

KW cancer; hyperproliferative disorder; human; HDGMR10; ligand; MCP-1.

XX

OS Homo sapiens.

XX

PN US2003166024-A1.

XX

PD 04-SEP-2003.

XX

PF 01-MAY-2002; 2002US-00135839.

XX

PR 09-FEB-2000; 2000US-0181258P.

PR 09-MAR-2000; 2000US-0187999P.

PR 22-SEP-2000; 2000US-0234336P.

PR 09-FEB-2001; 2001US-00779879.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Roschke V, Li Y, Ruben SM;  
 XX  
 DR WPI; 2003-898066/82.  
 XX  
 PT New polypeptide comprising domains of an antibody that binds G-protein  
 PT chemokine receptor CCR5 is useful to detect, diagnose, prognose or  
 PT monitor cancers and other hyperproliferative disorders and to treat or  
 PT prevent a disease or disorder.  
 XX  
 PS Disclosure; SEQ ID NO 9; 179pp; English.  
 XX  
 CC The invention describes a new isolated polynucleotide that encodes an  
 CC antibody (AB1) comprising an amino acid sequence of at least one, two or  
 CC three complementarity determining regions (CDR) of a heavy chain variable  
 CC (VH) domain of an antibody (AB2) that immunospecifically binds to a G-  
 CC protein chemokine receptor (CCR5), at least one, two or three CDR regions  
 CC of a light chain variable (VL) domain of AB2 or at least one, two or  
 CC three CDR regions of both a VH and a VL domain of AB2. The antibody is  
 CC useful for detecting, diagnosing, prognosing or monitoring cancers and  
 CC other hyperproliferative disorders and for treating, preventing or  
 CC ameliorating a disease or disorder. This is the amino acid sequence of  
 CC MCP-1, a ligand of human G protein chemokine receptor (CCR5) HDGMR10.  
 XX  
 SQ Sequence 344 AA;

Query Match 92.5%; Score 1823; DB 7; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-198;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	18	EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT	77
Db	1	EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT	60
Qy	78	DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID	137
Db	61	DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID	120
Qy	138	RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	197
Db	121	RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	180
Qy	198	WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT	257
Db	181	WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT	240
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	317
Db	241	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	300
Qy	318	IALGCRIAPLQKPVC GPGVRPGKNVKVTTQGLLDGRGKGKSIG	361
Db	301	IALGCRIAPLQKPVC GPGVRPGKNVKVTTQGLLDGRGKGKSIG	344

RESULT 11  
 ADP86217  
 ID ADP86217 standard; protein; 344 AA.

XX  
 AC ADP86217;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Human MCP-1 receptor protein.  
 XX  
 KW G-protein chemokine receptor; HDGNR10; CCR5; haematopoiesis;  
 KW wound healing; coagulation; angiogenesis; tumour; chronic infection;  
 KW leukaemia; T-cell mediated autoimmune diseases; parasitic infection;  
 KW psoriasis; allergy; anaphylaxis; atherogenesis; malignancy; inflammation;  
 KW prostaglandin-independent fever; bone marrow failure; silicosis;  
 KW sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome;  
 KW human; MCP-1 receptor ; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6743594-B1.  
 XX  
 PD 01-JUN-2004.  
 XX  
 PF 11-FEB-2000; 2000US-00502784.  
 XX  
 PR 06-JUN-1995; 95US-00466343.  
 PR 18-NOV-1998; 98US-00195662.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Li Y, Ruben SM;  
 XX  
 DR WPI; 2004-459648/43.  
 XX  
 PT Screening compounds binding to G-protein chemokine receptor HDGNR10,  
 PT involves contacting test compound with polypeptide of HDGRN10, and  
 PT observing binding of test compound to polypeptide.  
 XX  
 PS Disclosure; SEQ ID NO 9; 26pp; English.  
 XX  
 CC The invention relates to a method for screening compounds which bind the  
 CC G-protein chemokine receptor HDGNR10 (CCR5). Compounds identified by the  
 CC method of the invention are useful for stimulating haematopoiesis, wound  
 CC healing, coagulation, angiogenesis, for treating solid tumours, chronic  
 CC infections, leukaemia, T-cell mediated autoimmune diseases, parasitic  
 CC infections, psoriasis and for stimulating growth factor activity. The  
 CC compounds are also useful for treating allergy, anaphylaxis,  
 CC atherogenesis, malignancy, chronic and acute inflammation, histamine and  
 CC IgE-mediated allergic reactions, prostaglandin-independent fever, bone  
 CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis, shock and  
 CC hyper-eosinophilic syndrome. The present sequence is a human MCP-1  
 CC receptor protein. This sequence is used in the invention.  
 XX  
 SQ Sequence 344 AA;

Query Match 92.5%; Score 1823; DB 8; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-198;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy	18	EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT	77
Db	1	EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT	60
Qy	78	DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID	137
Db	61	DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID	120
Qy	138	RYLAIVHAVFALKARTVTTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	197
Db	121	RYLAIVHAVFALKARTVTTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	180
Qy	198	WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	257
Db	181	WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	240
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	317
Db	241	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	300
Qy	318	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG	361
Db	301	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG	344

RESULT 12

AAB46859

ID AAB46859 standard; protein; 329 AA.

XX

AC AAB46859;

XX

DT 16-AUG-2001 (revised)

DT 02-AUG-2001 (revised)

DT 04-MAY-2001 (first entry)

XX

DE Human MCP-1 receptor protein fragment.

XX

KW HDG NR10; human; G-protein chemokine receptor; antiinflammatory;  
KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;  
KW cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;  
KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;  
KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;  
KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;  
KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;  
KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;  
KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;  
KW hyper-eosinophilic syndrome; vulnerary.

XX

OS Homo sapiens.

XX

PN US2001000241-A1.

XX

PD 12-APR-2001.

XX

PF 29-NOV-2000; 2000US-00725285.

XX

PR 06-JUN-1995; 95US-00466343.

PR 18-NOV-1998; 98US-00195662.

PR 25-JUN-1999; 99US-00339912.

XX

PA (LIYY/) LI Y.

PA (RUBE/) RUBEN S M.

XX

PI Li Y, Ruben SM;

XX

DR WPI; 2001-226317/23.

XX

PT New human G-protein chemokine receptor polypeptides and polynucleotides,  
PT useful for identifying (ant)agonists to the G-protein chemokine receptor.

XX

PS Disclosure; Page 16-17; 22pp; English.

XX

CC This invention describes a novel receptor polypeptide (I) selected from  
CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the  
CC specification; and (ii) a polypeptide encoded by the cDNA contained in a  
CC plasmid, and fragments, analogs and derivatives of the polypeptide. The  
CC products of the invention have antiinflammatory, immunomodulatory,  
CC anticoagulant, antiallergic, immunosuppressive, vulnerary, cytostatic,  
CC antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic  
CC activity and can be used for gene therapy. The G-protein chemokine  
CC receptors, HDGMR10, (I) are useful for screening for compounds which  
CC activate or inhibit activation of (I). The products of the invention can  
CC also be used for stimulating haematopoiesis, wound healing, coagulation,  
CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-  
CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and  
CC stimulating growth factor activity. HDGMR10 is useful for treating  
CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute  
CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic  
CC reactions, prostaglandin-independent fever, bone marrow failure,  
CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-  
CC eosinophilic syndrome. (N.B. This record was resubmitted to correct  
CC errors in the keyword formatting)

XX

SQ Sequence 329 AA;

Query Match 87.7%; Score 1727.5; DB 4; Length 329;

Best Local Similarity 95.6%; Pred. No. 1.7e-187;

Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

```
Qy      18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
          |||
Db      1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy      78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
          |||
Db      61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105

Qy     138 RYLAIVHAVFALKARTVTTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
          |||
Db     106 RYLAIVHAVFALKARTVTTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy     198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRIFTIMIVYFLFWT 257
          |||
Db     166 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRIFTIMIVYFLFWT 225
```

QY 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317  
 |||  
 Db 226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285  
 QY 318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361  
 |||  
 Db 286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329

# RESULT 13

ABB81055

ID ABB81055 standard; protein; 329 AA.

XX

AC ABB81055;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human MCP-1 receptor.

XX

KW 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10;

KW G-protein chemokine receptor; haematopoietic; immunosuppressant;

KW antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic;

KW antirheumatic; antiarthritic; gene therapy; human; MCP-1; receptor.

XX

OS Homo sapiens.

XX

PN US2002076745-A1.

XX

PD 20-JUN-2002.

XX

PF 18-NOV-1998; 98US-00195662.

XX

PR 06-JUN-1995; 95US-00466343.

XX

PA (LIYY/) LI Y.

PA (RUBE/) RUBEN S M.

XX

PI Li Y, Ruben SM;

XX

DR WPI; 2002-598724/64.

XX

PT New polynucleotide encoding a human G protein chemokine receptor HDGNR10,

PT useful e.g. for treating tumors.

XX

PS Example; Fig 2; 22pp; English.

XX

CC The invention relates to a novel human 7-transmembrane receptor, HDGNR10,

CC which has been identified as a G-protein chemokine receptor. The GPCR

CC HDGNR10 polypeptide can be expressed by standard recombinant methodology.

CC Compounds that activate or inhibit the receptor polypeptide, optionally

CC expressed from DNA in gene therapy vectors, are used to treat diseases

CC that require: (a) activation of the receptor (e.g. stimulation of

CC haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune

CC diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the

CC receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis

CC etc). The present sequence represents a human MCP-1 receptor used in

CC comparison studies with the HDGMR10 receptor

XX

SQ Sequence 329 AA;

Query Match 87.7%; Score 1727.5; DB 5; Length 329;  
Best Local Similarity 95.6%; Pred. No. 1.7e-187;  
Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

```
Qy      18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
          |||
Db      1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy      78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
          |||
Db      61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105

Qy     138 RYLAIHVAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
          |||
Db     106 RYLAIHVAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy     198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
          |||
Db     166 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225

Qy     258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
          |||
Db     226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy     318 IALGCRIAPLQKPVC GPGVRPGKNVKVTTQGLLDGRGKGK SIG 361
          |||
Db     286 IALGCRIAPLQKPVC GPGVRPGKNVKVTTQGLLDGRGKGK SIG 329
```

#### RESULT 14

AAR79166

ID AAR79166 standard; protein; 360 AA.

XX

AC AAR79166;

XX

DT 25-MAR-2003 (revised)

DT 29-DEC-1995 (first entry)

XX

DE Human monocyte chemoattractant protein-1 receptor MCP-1RB.

XX

KW Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	Domain	1. .48
FT		/label= extracellular
FT	Domain	49. .70
FT		/label= transmembrane
FT	Domain	80. .700
FT		/label= transmembrane
FT	Domain	115. .136
FT		/label= transmembrane

FT Domain 154. .178  
 FT /label= transmembrane  
 FT Domain 204. .231  
 FT /label= transmembrane  
 FT Domain 244. .268  
 FT /label= transmembrane  
 FT Domain 295. .313  
 FT /label= transmembrane  
 FT Region 314. .360  
 FT /label= carboxyl tail  
 XX  
 PN WO9519436-A1.  
 XX  
 PD 20-JUL-1995.  
 XX  
 PF 11-JAN-1995; 95WO-US000476.  
 XX  
 PR 13-JAN-1994; 94US-00182962.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Charo I, Coughlin S;  
 XX  
 DR WPI; 1995-263866/34.  
 DR N-PSDB; AAQ96298.  
 XX  
 PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.  
 PT for identifying antagonists and for treating diseases characterised by  
 PT monocytic infiltrates.  
 XX  
 PS Claim 2; Fig 2; 84pp; English.  
 XX  
 CC To identify and clone new members of the chemokine receptor gene family,  
 CC degenerate oligo primers were designed corresp. to the conserved  
 CC sequences R79167 in the second and R79168 in the third transmembrane  
 CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the  
 CC HUMSTRS orphan receptor (GenBank Accession #M99293. The degenerate oligo  
 CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and  
 CC Q96300. Amplification of cDNA derived from MM6 cells with the primers  
 CC yielded a number of PCR products. One cDNA appeared to encode a novel  
 CC protein. To obtain a full-length version of this clone, a MM6 cDNA  
 CC library was constructed in pFROG and probed with the PCR product. A 2.1  
 CC kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA  
 CC library revealed a second sequence that was identical to the 2.1 kb cDNA  
 CC sequence first obtd. from the 5' UTR through the putative seventh  
 CC transmembrane domain but contained a different cytoplasmic tail. The  
 CC second sequence appears to represent alternative splicing of the carboxyl  
 CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-  
 CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-  
 CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.  
 CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 360 AA;

Query Match 83.8%; Score 1651.5; DB 2; Length 360;  
 Best Local Similarity 95.5%; Pred. No. 8.6e-179;

Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
      |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
      |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      |||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
      |||
Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPV 334

```

RESULT 15

AAW35833

ID AAW35833 standard; protein; 360 AA.

XX

AC AAW35833;

XX

DT 27-FEB-1998 (first entry)

XX

DE Human monocyte chemoattractant protein 1 receptor.

XX

KW Human; MCP-1; monocyte chemoattractant protein; receptor; tumour;  
 KW inflammatory disease; viral; allergy; diabetes.

XX

OS Homo sapiens.

XX

PN JP09238688-A.

XX

PD 16-SEP-1997.

XX

PF 11-MAR-1996; 96JP-00053574.

XX

PR 11-MAR-1996; 96JP-00053574.

XX

PA (TAKE ) TAKEDA CHEM IND LTD.

XX

DR WPI; 1997-506557/47.

DR N-PSDB; AAT96976.

XX

PT DNA encoding human monocyte chemoattractant protein 1 receptor - used to  
 PT treat tumours and inflammatory, viral, infectious, allergic, diabetic and

PT central nervous system diseases.  
 XX  
 PS Disclosure; Page 12-14; 15pp; Japanese.  
 XX  
 CC The present sequence represents human monocyte chemoattractant protein 1  
 CC (MCP-1) receptor protein. The MCP-1 receptor protein and encoding DNA are  
 CC used for the prevention and treatment of tumours and inflammatory, viral,  
 CC infectious, allergic, diabetic and central nervous system diseases  
 XX  
 SQ Sequence 360 AA;

Query Match 83.8%; Score 1651.5; DB 2; Length 360;  
 Best Local Similarity 95.5%; Pred. No. 8.6e-179;  
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFR---SLF---HIALG-CRIAPL	327
		:      :  :	
Db	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPV	334

Search completed: January 10, 2005, 11:30:23  
 Job time : 159 secs

OM protein - protein search, using sw model

Run on: January 10, 2005, 11:27:39 ; Search time 39 Seconds  
 (without alignments)  
 635.973 Million cell updates/sec

Title: US-10-791-592-2  
 Perfect score: 1970  
 Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	1970	100.0	374	1	US-08-450-393A-2	Sequence 2, Appli
2	1970	100.0	374	3	US-08-446-669-2	Sequence 2, Appli
3	1970	100.0	374	4	US-10-039-659A-14	Sequence 14, Appli
4	1970	100.0	374	4	US-09-625-573-2	Sequence 2, Appli
5	1970	100.0	374	5	PCT-US95-00476-2	Sequence 2, Appli
6	1823	92.5	344	3	US-08-466-343D-9	Sequence 9, Appli
7	1823	92.5	344	4	US-09-502-784A-9	Sequence 9, Appli
8	1727.5	87.7	329	4	US-09-502-783A-9	Sequence 9, Appli
9	1727.5	87.7	329	4	US-09-339-912A-9	Sequence 9, Appli
10	1651.5	83.8	360	1	US-08-450-393A-4	Sequence 4, Appli
11	1651.5	83.8	360	3	US-08-446-669-4	Sequence 4, Appli



12	1651.5	83.8	360	3	US-09-045-583-50	Sequence 50, Appl
13	1651.5	83.8	360	4	US-09-534-185-50	Sequence 50, Appl
14	1651.5	83.8	360	4	US-09-131-827A-2	Sequence 2, Appli
15	1651.5	83.8	360	4	US-09-625-573-4	Sequence 4, Appli
16	1651.5	83.8	360	5	PCT-US95-00476-4	Sequence 4, Appli
17	1650.5	83.8	360	4	US-09-131-827A-20	Sequence 20, Appl
18	1645.5	83.5	360	4	US-08-833-752-7	Sequence 7, Appli
19	1645.5	83.5	360	4	US-09-938-719-7	Sequence 7, Appli
20	1614.5	82.0	360	3	US-09-045-583-51	Sequence 51, Appl
21	1614.5	82.0	360	4	US-09-534-185-51	Sequence 51, Appl
22	1589.5	80.7	347	1	US-08-461-244-3	Sequence 3, Appli
23	1236	62.7	352	3	US-09-517-605-5	Sequence 5, Appli
24	1234	62.6	354	3	US-08-724-984A-2	Sequence 2, Appli
25	1230	62.4	352	3	US-09-045-583-52	Sequence 52, Appl
26	1230	62.4	352	4	US-09-534-185-52	Sequence 52, Appl
27	1224	62.1	352	3	US-09-087-232A-13	Sequence 13, Appl
28	1224	62.1	352	3	US-08-861-105-14	Sequence 14, Appl
29	1224	62.1	352	3	US-08-575-967A-2	Sequence 2, Appli
30	1224	62.1	352	4	US-08-833-752-5	Sequence 5, Appli
31	1224	62.1	352	4	US-09-502-783A-2	Sequence 2, Appli
32	1224	62.1	352	4	US-09-796-202-1	Sequence 1, Appli
33	1224	62.1	352	4	US-09-938-719-5	Sequence 5, Appli
34	1224	62.1	352	4	US-09-502-784A-2	Sequence 2, Appli
35	1224	62.1	352	4	US-09-339-912A-2	Sequence 2, Appli
36	1224	62.1	352	4	US-08-771-276-2	Sequence 2, Appli
37	1224	62.1	352	4	US-08-771-276-20	Sequence 20, Appl
38	1215	61.7	352	3	US-08-466-343D-2	Sequence 2, Appli
39	967.5	49.1	355	1	US-08-012-988A-2	Sequence 2, Appli
40	967.5	49.1	355	1	US-08-450-393A-5	Sequence 5, Appli
41	967.5	49.1	355	3	US-08-446-669-5	Sequence 5, Appli
42	967.5	49.1	355	3	US-09-239-938-1	Sequence 1, Appli
43	967.5	49.1	355	4	US-09-886-319A-14	Sequence 14, Appl
44	967.5	49.1	355	4	US-10-039-659A-13	Sequence 13, Appl
45	967.5	49.1	355	4	US-09-961-068-1	Sequence 1, Appli

#### ALIGNMENTS

##### RESULT 1

US-08-450-393A-2

; Sequence 2, Application US/08450393A

; Patent No. 5707815

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-2

```

```

Query Match          100.0%; Score 1970; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.1e-150;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
        ||||||||||||
Db    361 GRAPEASLQDKEGA 374

```

RESULT 2

US-08-446-669-2

; Sequence 2, Application US/08446669

; Patent No. 6132987

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,669

; FILING DATE: May 25, 1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Neeley, Richard

; REGISTRATION NUMBER: 30,092

; REFERENCE/DOCKET NUMBER: UCAL-237/01US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-843-5000

; TELEFAX: 415-857-0663

; TELEX: 380816CooleyPA

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 374 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-446-669-2

Query Match 100.0%; Score 1970; DB 3; Length 374;

Best Local Similarity 100.0%; Pred. No. 4.1e-150;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY 120
        |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

```

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240  
 |||  
 Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300  
 |||  
 Db 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360  
 |||  
 Db 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy 361 GRAPEASLQDKEGA 374  
 |||  
 Db 361 GRAPEASLQDKEGA 374

RESULT 3

US-10-039-659A-14

; Sequence 14, Application US/10039659A  
 ; Patent No. 6723520  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Wei  
 ; APPLICANT: Gish, Kurt C.  
 ; APPLICANT: Schall, Thomas J.  
 ; APPLICANT: Vicari, Alain P.  
 ; APPLICANT: Zlotnik, Albert  
 ; TITLE OF INVENTION: Antibodies that bind chemokine TECK  
 ; FILE REFERENCE: DX0589K1B US  
 ; CURRENT APPLICATION NUMBER: US/10/039,659A  
 ; CURRENT FILING DATE: 2002-01-03  
 ; PRIOR APPLICATION NUMBER: US 08/887,977  
 ; PRIOR FILING DATE: 1997-07-03  
 ; PRIOR APPLICATION NUMBER: US 60/021,664  
 ; PRIOR FILING DATE: 1996-07-05  
 ; PRIOR APPLICATION NUMBER: US 60/028,329  
 ; PRIOR FILING DATE: 1996-10-11  
 ; PRIOR APPLICATION NUMBER: US 60/048,593  
 ; PRIOR FILING DATE: 1997-06-04  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 14  
 ; LENGTH: 374  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-039-659A-14

Query Match 100.0%; Score 1970; DB 4; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-150;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60  
 |||  
 Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

```

      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy      241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy      301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy      361 GRAPEASLQDKEGA 374
      ||||||||||||||||
Db      361 GRAPEASLQDKEGA 374

```

RESULT 4

US-09-625-573-2

; Sequence 2, Application US/09625573

; Patent No. 6730301

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/625,573

; FILING DATE: 25-Jul-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,669

; FILING DATE: May 25, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Neeley, Richard

; REGISTRATION NUMBER: 30,092

; REFERENCE/DOCKET NUMBER: UCAL-237/01US

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-625-573-2

```

```

Query Match          100.0%; Score 1970; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.1e-150;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
        |||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
        |||
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
        |||
Db    361 GRAPEASLQDKEGA 374

```

# RESULT 5

PCT-US95-00476-2

; Sequence 2, Application PC/TUS9500476

## ; GENERAL INFORMATION:

```

; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor

```

```

;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90012-2628
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/00476
;      FILING DATE:
;      CLASSIFICATION:
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Berliner, Robert
;      REGISTRATION NUMBER:  20,121
;      REFERENCE/DOCKET NUMBER:  5555-291
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  310-977-1001
;      TELEFAX:  310-977-1003
;      TELEX:
;      INFORMATION FOR SEQ ID NO:  2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  374 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
PCT-US95-00476-2

```

```

Query Match          100.0%;  Score 1970;  DB 5;  Length 374;
Best Local Similarity 100.0%;  Pred. No. 4.1e-150;
Matches 374;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|
Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|
Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|
Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
|
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
|
Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
|
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
|
Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
|
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
|

```

Qy 361 GRAPEASLQDKEGA 374  
|||||||  
Db 361 GRAPEASLQDKEGA 374

RESULT 6

US-08-466-343D-9

; Sequence 9, Application US/08466343D

; Patent No. 6025154

; GENERAL INFORMATION:

; APPLICANT: LI, Yi

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN

; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDG NR10 (AS AMENDED)

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVE., NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/466,343D

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: STEFFE, ERIC K.

; REGISTRATION NUMBER: 36,688

; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 344 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-466-343D-9

Query Match 92.5%; Score 1823; DB 3; Length 344;

Best Local Similarity 100.0%; Pred. No. 2.2e-138;

Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77  
|||||

Db 1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 137  
|||||

Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 120



Qy	138	RYLAIVHAVFALKARTVTFGVVT	SVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	197
Db	121	RYLAIVHAVFALKARTVTFGVVT	SVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	180
Qy	198	WNNFHTIMRNILGLVLP	LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	257
Db	181	WNNFHTIMRNILGLVLP	LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	240
Qy	258	PYNIVILLNTFQEFFGLSNCESTS	QLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	317
Db	241	PYNIVILLNTFQEFFGLSNCESTS	QLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	300
Qy	318	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG		361
Db	301	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG		344

RESULT 7

US-09-502-784A-9

```

; Sequence 9, Application US/09502784A
; Patent No. 6743594
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Methods of Screening Using Human G-Protein
; TITLE OF INVENTION: Chemokine Receptor HDGNR10 (CCR5)
; FILE REFERENCE: 1488.1150005
; CURRENT APPLICATION NUMBER: US/09/502,784A
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-502-784A-9

```

```

Query Match          92.5%; Score 1823; DB 4; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-138;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy	18	EEVTTFFDYDYGAPCHKFDVKQIGAQLLP	PLYSLVFIFGFVGNMLVVLILINCKKLKCLT	77
Db	1	EEVTTFFDYDYGAPCHKFDVKQIGAQLLP	PLYSLVFIFGFVGNMLVVLILINCKKLKCLT	60
Qy	78	DIYLLNLAISDLLFLITLPLWAHSAANEWV	FGNAMCKLFTGLYHIGYFGGIFFIILLTID	137
Db	61	DIYLLNLAISDLLFLITLPLWAHSAANEWV	FGNAMCKLFTGLYHIGYFGGIFFIILLTID	120
Qy	138	RYLAIVHAVFALKARTVTFGVVT	SVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	197
Db	121	RYLAIVHAVFALKARTVTFGVVT	SVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	180

Qy	198	WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	257
Db	181	WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	240
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	317
Db	241	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	300
Qy	318	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG	361
Db	301	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG	344

RESULT 8

US-09-502-783A-9

; Sequence 9, Application US/09502783A

; Patent No. 6511826

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)

; TITLE OF INVENTION: HDGNR10

; FILE REFERENCE: 1488.1150006

; CURRENT APPLICATION NUMBER: US/09/502,783A

; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: 08/466,343

; PRIOR FILING DATE: 1995-06-06

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9

; LENGTH: 329

; TYPE: PRT

; ORGANISM: Protein

US-09-502-783A-9

Query Match 87.7%; Score 1727.5; DB 4; Length 329;  
 Best Local Similarity 95.6%; Pred. No. 9.1e-131;  
 Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

Qy	18	EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT	77
Db	1	EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT	60
Qy	78	DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID	137
Db	61	DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI-----	105
Qy	138	RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	197
Db	106	RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	165
Qy	198	WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	257
Db	166	WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	225

Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317  
 |||  
 Db 226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy 318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361  
 |||  
 Db 286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329

RESULT 9

US-09-339-912A-9

; Sequence 9, Application US/09339912A  
 ; Patent No. 6759519  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Yi  
 ; APPLICANT: Ruben, Steven, M.  
 ; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor  
 HDGNR10  
 ; TITLE OF INVENTION: (CCR5 Receptor)  
 ; FILE REFERENCE: 1488.1150003  
 ; CURRENT APPLICATION NUMBER: US/09/339,912A  
 ; CURRENT FILING DATE: 1999-06-25  
 ; PRIOR APPLICATION NUMBER: 09/195,662  
 ; PRIOR FILING DATE: 1998-11-18  
 ; PRIOR APPLICATION NUMBER: 08/466,343  
 ; PRIOR FILING DATE: 1995-06-06  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 329  
 ; TYPE: PRT  
 ; ORGANISM: Protein  
 US-09-339-912A-9

Query Match 87.7%; Score 1727.5; DB 4; Length 329;  
 Best Local Similarity 95.6%; Pred. No. 9.1e-131;  
 Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

Qy 18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77  
 |||  
 Db 1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137  
 |||  
 Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105

Qy 138 RYLAIVHAVFALKARTVTFGVVT SVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197  
 |||  
 Db 106 RYLAIVHAVFALKARTVTFGVVT SVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy 198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRVIFTIMIVYFLFWT 257  
 |||  
 Db 166 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRVIFTIMIVYFLFWT 225

Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317  
 |||  
 Db 226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy            318 IALGCRIAPLQKPVCGGPGVPRGKNVKVTTQGLLDGRGKGKSIG 361  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db            286 IALGCRIAPLQKPVCGGPGVPRGKNVKVTTQGLLDGRGKGKSIG 329

RESULT 10

US-08-450-393A-4

; Sequence 4, Application US/08450393A

; Patent No. 5707815

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

TITLE OF INVENTION: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

```
;      MEDIUM TYPE:  Floppy disk
```

```

;      COMPUTER:  IBM PC compatible

```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/450,393A

FILING DATE: May 25, 1995

CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Cserr, Luann

REGISTRATION NUMBER: 31,822

REFERENCE/DOCKET NUMBER: UCAL-237/02US

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-843-5165

; TELEFAX: 415-8857-0663

; TELEX: 380816CooleyPA

; INFORMATION FOR SEO ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids

```
;      TYPE:  amino acid
```

```
;      TOPOLOGY:  linear
```

```
; MOLECULE TYPE:  protein
```

US-08-450-393A-4

Query Match 83.8%; Score 1651.5; DB 1; Length 360;

Best Local Similarity 95.5%; Pred. No. 1.2e-124;

Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

\_\_\_\_\_

Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

```

      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLMVICYSGILKTLLRCRNEKKRHR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLMVICYSGILKTLLRCRNEKKRHR 240

Qy      241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy      301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
      ||||||||||||  |:|  ||  |:  |:
Db      301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPV 334

```

RESULT 11

US-08-446-669-4

; Sequence 4, Application US/08446669

; Patent No. 6132987

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,669

; FILING DATE: May 25, 1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Neeley, Richard

; REGISTRATION NUMBER: 30,092

; REFERENCE/DOCKET NUMBER: UCAL-237/01US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-843-5000

; TELEFAX: 415-857-0663

; TELEX: 380816CooleyPA

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-446-669-4

Query Match 83.8%; Score 1651.5; DB 3; Length 360;  
Best Local Similarity 95.5%; Pred. No. 1.2e-124;  
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
        |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
        |||
Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQKQCPV 334
```

RESULT 12

US-09-045-583-50

; Sequence 50, Application US/09045583  
; Patent No. 6287805  
; GENERAL INFORMATION:  
; APPLICANT: Graham, Gerard J. et al.  
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/045,583  
; FILING DATE: 20-MAR-98

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-50

```

```

Query Match          83.8%; Score 1651.5; DB 3; Length 360;
Best Local Similarity 95.5%; Pred. No. 1.2e-124;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

```

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
        |||||||||||| |:| || |: |:
Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPV 334

```

RESULT 13

US-09-534-185-50

```

; Sequence 50, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses

```

```

;                               Therefor
;   NUMBER OF SEQUENCES: 56
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: LAHIVE & COCKFIELD, LLP
;       STREET: 28 State Street
;       CITY: Boston
;       STATE: Massachusetts
;       COUNTRY: USA
;       ZIP: 02109
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/534,185
;       FILING DATE: 24-Mar-2000
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 09/045,583
;       FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Mandragouras, Amy E.
;       REGISTRATION NUMBER: 36,207
;       REFERENCE/DOCKET NUMBER: MNI-044
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (617)227-7400
;       TELEFAX: (617)742-4214
;   INFORMATION FOR SEQ ID NO: 50:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 360 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       FRAGMENT TYPE: internal
;       SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

```

```

Query Match          83.8%; Score 1651.5; DB 4; Length 360;
Best Local Similarity 95.5%; Pred. No. 1.2e-124;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

```

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

```



```

Qy      241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |||
Db      241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy      301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
        |||
Db      301 NPIIYAFVGEKFRRYLSVFFRKHITKRFECKQCPV 334

```

RESULT 14

US-09-131-827A-2

```

; Sequence 2, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-2

```

```

Query Match      83.8%; Score 1651.5; DB 4; Length 360;
Best Local Similarity 95.5%; Pred. No. 1.2e-124;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

```

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
        |||
Db      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy      121 HIGYFGGIIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db      121 HIGYFGGIIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy      241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |||
Db      241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

```

```
Qy      301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327  
        ||||| | :|   ||   |:  |:  
Db      301 NPIIYAFVGEKFRRYLSVFRRKHITKRFCCKOCPV 334
```

RESULT 15

US-09-625-573-4

; Sequence 4, Application US/09625573

; Patent No. 6730301

## ; GENERAL INFORMATION:

APPLICANT: Charo, Israel

; Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
 ; PROTEIN RECEPTORS

```

;          NUMBER OF SEQUENCES: 14

```

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Floppy disk
```

```

;               COMPUTER: IBM PC compatible

```

```
;      OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```
;      CURRENT APPLICATION DATA:
```

; APPLICATION NUMBER: US/09/625,573

; FILING DATE: 25-Jul-2000

; CLASSIFICATION: <Unknown>

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,669

FILING DATE: May 25, 1995

ATTORNEY/AGENT INFORMATION:

```
;      NAME: Neeley, Richard
```

REGISTRATION NUMBER: 30,092

REFERENCE/DOCKET NUMBER: UCAL-237/01US

## ; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-843-5000

; TELEFAX: 415-857-0663

; TELEX: 380816CooleyPA

## ; INFORMATION FOR SEQ ID NO: 4:

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids

```
;          TYPE: amino acid
```

```
;          TOPOLOGY: linear
```

; MOLECULE TYPE: protein

```

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

US-09-625-573-4

Query Match 83.8%; Score 1651.5; DB 4; Length 360;

Best Local Similarity 95.5%; Pred. No. 1.2e-124;

Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60

Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFR---SLF---HIALG-CRIAPL	327
Db	301	NPIIYAFVGEKFRRLSVFFRKHITKRFCQCPV	334

Search completed: January 10, 2005, 11:34:25  
Job time : 41 secs

OM protein - protein search, using sw model

Run on: January 10, 2005, 11:27:39 ; Search time 40 Seconds  
 (without alignments)  
 899.627 Million cell updates/sec

Title: US-10-791-592-2  
 Perfect score: 1970  
 Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_79:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1970	100.0	374	2	I38450	chemokine (C-C) re
2	1651.5	83.8	360	2	JC2443	chemokine (C-C) re
3	1224	62.1	352	2	A43113	chemokine (C-C) re
4	967.5	49.1	355	2	A45177	chemokine (C-C) re
5	960	48.7	359	2	I49341	MIP-1 alpha recept
6	902.5	45.8	355	2	I49339	macrophage inflamm
7	890.5	45.2	355	2	G02436	chemokine (C-C) re
8	833	42.3	360	2	JC4587	chemokine (C-C) re
9	831.5	42.2	360	2	A57160	chemokine (C-C) re
10	794.5	40.3	383	2	S55594	G protein-coupled
11	731	37.1	356	2	I49340	MIP-1 alpha recept
12	723	36.7	355	2	JC5067	G protein-coupled
13	704.5	35.8	354	2	I58186	probable G protein

14	698	35.4	355	2	JC4304	orphan G protein-c
15	644.5	32.7	344	2	JC5942	chemokine receptor
16	584	29.6	378	2	B55735	lymphocyte-specifi
17	575.5	29.2	378	2	A55735	G protein-coupled
18	570	28.9	378	2	A45680	G protein-coupled
19	554.5	28.1	369	2	JC5068	G protein-coupled
20	541.5	27.5	360	2	A53611	interleukin-8 rece
21	537	27.3	359	2	A48921	interleukin-8 rece
22	531	27.0	352	2	G00048	fusin (LESTRA) - c
23	530.5	26.9	353	2	S28787	neuropeptide Y/pep
24	529.5	26.9	355	2	JQ1231	interleukin-8 rece
25	528	26.8	352	2	A45747	neuropeptide Y/pep
26	526	26.7	358	2	A53752	interleukin-8 rece
27	526	26.7	367	2	JE0349	interferon-inducib
28	524.5	26.6	350	2	A39445	interleukin-8 rece
29	523	26.5	356	2	S42096	interleukin-8 rece
30	519	26.3	333	2	I65989	G protein-coupled
31	484	24.6	350	2	JN0621	G protein-coupled
32	480	24.4	359	2	A42656	angiotensin II rec
33	479.5	24.3	374	2	S42628	G protein-coupled
34	475	24.1	359	2	I51372	angiotensin II rec
35	473	24.0	359	2	JC2134	angiotensin II rec
36	472	24.0	359	2	JH0621	angiotensin II rec
37	471	23.9	359	2	S15403	angiotensin II rec
38	471	23.9	359	2	JQ1516	angiotensin II rec
39	469	23.8	359	2	JC1104	angiotensin II rec
40	468	23.8	359	2	S44425	angiotensin II rec
41	465	23.6	359	2	JC1194	angiotensin II rec
42	465	23.6	374	2	S32785	G protein-coupled
43	464	23.6	359	2	A48857	angiotensin II rec
44	461.5	23.4	372	2	S26667	G protein-coupled
45	460.5	23.4	327	2	S56162	MDCR15 protein - h

# ALIGNMENTS

## RESULT 1

I38450

chemokine (C-C) receptor 2, splice form A - human

N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemotactin 1 receptor

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 09-Jul-2004

C;Accession: I38450

\* R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.

A;Reference number: A53477; MUID:94195821; PMID:8146186

A;Accession: I38450

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-374 <RES>

A;Cross-references: UNIPROT:P41597; EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556

C;Genetics:

A;Gene: GDB:CMKBR2

A;Cross-references: GDB:337364; OMIM:601267

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

F;44-68/Domain: transmembrane #status predicted <TM1>

F;79-99/Domain: transmembrane #status predicted <TM2>

F;115-136/Domain: transmembrane #status predicted <TM3>

F;154-178/Domain: transmembrane #status predicted <TM4>

F;208-226/Domain: transmembrane #status predicted <TM5>

F;244-265/Domain: transmembrane #status predicted <TM6>

F;292-309/Domain: transmembrane #status predicted <TM7>

F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;32-277,113-190/Disulfide bonds: #status predicted

Query Match 100.0%; Score 1970; DB 2; Length 374;

Best Local Similarity 100.0%; Pred. No. 1e-164;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
          |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
          |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
          |||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
          |||
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
          |||
Db    361 GRAPEASLQDKEGA 374
```

## RESULT 2

JC2443

chemokine (C-C) receptor 2, splice form B - human

N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemotactin 1 receptor

C;Species: Homo sapiens (man)  
 C;Date: 21-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004  
 C;Accession: JC2443; I38463  
 \* R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.  
 Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994  
 A;Title: cDNA cloning and functional expression of a human monocyte  
 chemoattractant protein 1 receptor.  
 A;Reference number: JC2443; MUID:94324942; PMID:8048929  
 A;Accession: JC2443  
 A;Molecule type: mRNA  
 A;Residues: 1-360 <YAM>  
 A;Cross-references: UNIPROT:P41597; DDBJ:D29984; NID:g531246; PIDN:BAA06253.1;  
 PID:g531247  
 R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin,  
 S.R.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
 A;Title: Molecular cloning and functional expression of two monocyte  
 chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-  
 terminal tails.  
 A;Reference number: A53477; MUID:94195821; PMID:8146186  
 A;Accession: I38463  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-360 <RES>  
 A;Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558  
 C;Genetics:  
 A;Gene: GDB:CMKBR2  
 A;Cross-references: GDB:337364; OMIM:601267  
 A;Map position: 3p21-3p21  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein;  
 transmembrane protein  
 F;43-70/Domain: transmembrane #status predicted <TM1>  
 F;81-100/Domain: transmembrane #status predicted <TM2>  
 F;115-136/Domain: transmembrane #status predicted <TM3>  
 F;154-178/Domain: transmembrane #status predicted <TM4>  
 F;207-226/Domain: transmembrane #status predicted <TM5>  
 F;244-268/Domain: transmembrane #status predicted <TM6>  
 F;287-309/Domain: transmembrane #status predicted <TM7>  
 F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;113-190/Disulfide bonds: #status predicted

Query Match 83.8%; Score 1651.5; DB 2; Length 360;  
 Best Local Similarity 95.5%; Pred. No. 7.1e-137;  
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180

```

Qy      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240
          |||
Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240

Qy      241 AVRVI FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
          |||
Db      241 AVRVI FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300

Qy      301 NP IIYAFVGEKFR---SLF---HIALG-CRIAPL 327
          |||
Db      301 NP IIYAFVGEKFR RYLSVFFRK HITKR FCKQCPV 334

```

# RESULT 3

A43113

chemokine (C-C) receptor 5 - human

N;Alternate names: C-C CKR-5; CCR5

C;Species: Homo sapiens (man)

C;Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 20-Jun-2000

C;Accession: A43113; S71808; A58834; A58832; G02653; A58833

R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.

Biochemistry 35, 3362-3367, 1996

A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor gene.

A;Reference number: A43113; MUID:96241590; PMID:8639485

A;Accession: A43113

A;Molecule type: mRNA

A;Residues: 1-352 <SAM1>

A;Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811

R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.;

Saragosti, S.; Lapoumeroulie, C.; Cognaux, J.; Forceille, C.; Muyldermans, G.;

Verhofstede, C.; Burtonboy, G.; Georges, M.; Imai, T.; Rana, S.; Yi, Y.; Smyth,

R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Parmentier, M.

Nature 382, 722-725, 1996

A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the CCR-5 chemokine receptor gene.

A;Reference number: S71808; MUID:96345670; PMID:8751444

A;Accession: S71808

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 182-206;207-230 <SAM2>

A;Accession: A58834

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-184, 'IKDSHLGAGPAAACHGHLLLG NPKNSASVSK' <SAM3>

A;Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063

A;Note: this frameshift mutation results in a non-functional receptor but confers a degree of resistance to HIV-1 infection; it has an allele frequency of 0.09 or more in some caucasian populations and may have had a selective advantage by conferring resistance to Yersinia plague infections

R;Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.

J. Leukoc. Biol. 60, 147-152, 1996

A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor selective for MIP-1alpha, MIP-1beta, and RANTES.



A;Reference number: A58832; MUID:96295970; PMID:8699119  
 A;Accession: A58832  
 A;Molecule type: mRNA  
 A;Residues: 1-352 <COM1>  
 A;Cross-references: GB:U57840; NID:gl502408; PIDN:AAB17071.1; PID:gl502409  
 A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes  
 R;Combadiere, C.  
 submitted to the EMBL Data Library, May 1996  
 A;Reference number: H01541  
 A;Accession: G02653  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-89,'L',91-352 <COM2>  
 A;Cross-references: EMBL:U57840  
 R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.  
 J. Biol. Chem. 271, 17161-17166, 1996  
 A;Title: Molecular cloning and functional characterization of a novel human CC  
 chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.  
 A;Reference number: A58833; MUID:96291862; PMID:8663314  
 A;Accession: A58833  
 A;Molecule type: mRNA  
 A;Residues: 1-352 <RAP>  
 A;Cross-references: GB:U54994; NID:gl457945; PIDN:AAC50598.1; PID:gl457946  
 C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-  
 1beta (see PIR:A31767), and RANTES (see PIR:A28815).  
 C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of  
 chemokine (C-C) receptor 5 and T-cell surface glycoprotein CD4 (see PIR:RWHUT4).  
 C;Genetics:  
 A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13  
 A;Cross-references: GDB:1230510; OMIM:601373  
 A;Map position: 3p21-3p21  
 C;Function:  
 A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta  
 and RANTES  
 A;Note: probably acts to control granulocyte proliferation and differentiation  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein;  
 transmembrane protein  
 F;32-56/Domain: transmembrane #status predicted <TM1>  
 F;67-87/Domain: transmembrane #status predicted <TM2>  
 F;103-124/Domain: transmembrane #status predicted <TM3>  
 F;142-166/Domain: transmembrane #status predicted <TM4>  
 F;193-218/Domain: transmembrane #status predicted <TM5>  
 F;236-257/Domain: transmembrane #status predicted <TM6>  
 F;285-300/Domain: transmembrane #status predicted <TM7>  
 F;20-269,101-178/Disulfide bonds: #status predicted  
 F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted  
 F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 62.1%; Score 1224; DB 2; Length 352;  
 Best Local Similarity 76.3%; Pred. No. 1.8e-99;  
 Matches 235; Conservative 27; Mismatches 34; Indels 12; Gaps 3;

Qy	24	FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL	81
		:  :       :     :       :       :	
Db	10	YDINYTTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL	69

Qy 82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTIDRYLA 141  
 ||||| ||:| || | : | || | : | || | : | ||||| |||||  
 Db 70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIIFFIILLTIDRYLA 129

Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197  
 :|||:|||||:|||||:|||||: || | : || :  
 Db 130 VHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSSHPYSQYQF 189

Qy 198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRVRIFTIMIVYFLFWT 257  
 | || | : |||||:|||||:|||||:|||||:|||||:|||||  
 Db 190 WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRVRLIFTIMIVYFLFWA 249

Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316  
 ||||:|||||:|| | :::||| |||||:|||||:|||||:|||||:|||||:|||||  
 Db 250 PYNIVLLLNTFQEFFGLNNCSSNRDLQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309

Qy 317 -----HIA 319  
 |||  
 Db 310 VFFQKHIA 317

#### RESULT 4

A45177

chemokine (C-C) receptor 1 - human

N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004

C;Accession: A45177; I55671

R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.

Cell 72, 415-425, 1993

A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor.

A;Reference number: A45177; MUID:93161416; PMID:7679328

A;Accession: A45177

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-355 <NEO>

A;Cross-references: UNIPROT:P32246; GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

A;Experimental source: HL60 cells

A;Note: sequence extracted from NCBI backbone (NCBIP:124876)

R;Gao, J.

J. Exp. Med. 177, 1421-1427, 1993

A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha (MIP-1alpha)/RANTES receptor.

A;Reference number: I55671; MUID:93240122; PMID:7683036

A;Accession: I55671

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-355 <RES>

A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

C;Genetics:

A;Gene: GDB:CMKBR1; CMKR-1

A;Cross-references: GDB:138446; OMIM:601159

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein  
 F;36-60/Domain: transmembrane #status predicted <TM1>  
 F;71-91/Domain: transmembrane #status predicted <TM2>  
 F;108-129/Domain: transmembrane #status predicted <TM3>  
 F;147-171/Domain: transmembrane #status predicted <TM4>  
 F;205-223/Domain: transmembrane #status predicted <TM5>  
 F;240-264/Domain: transmembrane #status predicted <TM6>  
 F;288-305/Domain: transmembrane #status predicted <TM7>  
 F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;24-273,106-183/Disulfide bonds: #status predicted  
 F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 49.1%; Score 967.5; DB 2; Length 355;  
 Best Local Similarity 58.7%; Pred. No. 4.9e-77;  
 Matches 185; Conservative 47; Mismatches 72; Indels 11; Gaps 5;

Qy	12	NTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCK	71
		:               : :                 :       :       :	
Db	5	NTTED-YDTTTEFDYGDATPCQKVNERAFGAQLLPPLYSLVFVIGLVGNILVVLVLVQYK	63
Qy	72	KLKCLTDIYLLNLAISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIF	130
		:     :                         : :       :       :       :	
Db	64	RLKNMTSIYLLNLAISDLLFLFTLPFWIDYKLKDDWVFGDAMCKILSGFYTGlySEIFF	123
Qy	131	IILLTIDRYLAIVHAVFALKARTVTFGVTVSVITWLVAVFASVPGIIFTKCQKEDSVYVC	190
		:           :     :     :     :	
Db	124	IILLTIDRYLAIVHAVFALRARTVTFGVITSIIWALAILASMPGLYFSKTQWEFTHTC	183
Qy	191	GPYFP----RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRVAVRVIF	246
		:             :   :   :         :       :       :       :	
Db	184	SLHFPHESLREWKLQALKNLFGVLVPLLVMIICYTGIIKILLRRPNEKK-SKAVRLIF	242
Qy	247	TIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYA	306
		:             :     :     :       :       :       :	
Db	243	VIMIIFFLFWTPYNLTLISVFDLFTHECEQSRHLDLAVQVTEVIAYTHCCVNPVIYA	302
Qy	307	FVGEKF----RSLFH	317
		:	
Db	303	FVGERFRKYLRQLFH	317

# RESULT 5

I49341

MIP-1 alpha receptor like-2 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: I49341

R;Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.

A;Reference number: I49339; MUID:95340546; PMID:7542241

A;Accession: I49341

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA  
A;Residues: 1-359 <RES>  
A;Cross-references: UNIPROT:Q8K3M7; EMBL:U28406; NID:g881551; PID:g881552  
C;Superfamily: vertebrate rhodopsin

Query Match 48.7%; Score 960; DB 2; Length 359;  
Best Local Similarity 50.1%; Pred. No. 2.2e-76;  
Matches 187; Conservative 59; Mismatches 89; Indels 38; Gaps 7;

```
Qy      10 IRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILIN 69
      |:  || |  || :|:: || |  :|::|: ||||| || |  :||:|||||
Db      8 IKTVVESFE--TTPYEYEWAPPCEKVRikelGSWLLPPLYSLVFIIGLLGNMMVVLILIK 65

Qy      70 CKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAA-NEWVFGNAMCKLFTGLYHIGYFGGI 128
      :||: :|:| | ||||| || |  || |  || |  ||: :| |:: : |
Db      66 YRKLQIMTNIYLFNLAI SDLLFLFTVPFWIHVVLWNEWGFGHYMCKMLSGFYLLALYSEI 125

Qy     129 FFIILLTIDRYLAIVHAVFALKARTVTFGVTVSVITWLVAVFASVPGIIFTKCQKEDSVY 188
      ||||| ||||| ||||| :||| |  :||: || |  ||: |  || : |  :
Db     126 FFIILLTIDRYLAIVHAVFALRARTVTFATITSIITWGLAGLALPEFIFHESQDSFGEF 185

Qy     189 VCGPYFPRG----WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRV 244
      | | :| |  | || : || | |||: ||||| :||| |  ||:|:|:|
Db     186 SCSPRYPEGEEDSWKRFHALRMNIFGLALPLLVMVICYSGIIKTLLRCPN-KKKHKAIRL 244

Qy     245 IFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPII 304
      || :||:|:| ||||| :|: |  |  :||: |  || | ||| :  |||:|:|
Db     245 IFVVMIVFFIFWTPYNLVLLFSAFHSTFLETSCQSKHLDLAMQVTEVIAYTHCCVNPVI 304

Qy     305 YAFVGEKFRS----LFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGL---LDGRGKG 357
      |||||:| |  ||  :||: | : : | | |
Db     305 YAFVGERFRKHLRLFFH-----RNVQFTWENIFQFLPGEENG 341

Qy     358 KSIGRAPEASLQD 370
      :: :| | :
Db     342 RTSSVSPSTGEQE 354
```

#### RESULT 6

I49339

macrophage inflammatory protein-1 alpha receptor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: I49339

R;Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.

A;Reference number: I49339; MUID:95340546; PMID:7542241

A;Accession: I49339

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-355 <RES>

A;Cross-references: UNIPROT:P51675; EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548

C;Superfamily: vertebrate rhodopsin

Query Match 45.8%; Score 902.5; DB 2; Length 355;  
 Best Local Similarity 53.1%; Pred. No. 2.4e-71;  
 Matches 170; Conservative 58; Mismatches 75; Indels 17; Gaps 6;

```

Qy      21 TTFDDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIY 80
      || |||  || | |: || ||||| ||| | |||:|:|:|: :|:|: ||
Db      13 TTEFDYGDSTPCQKTAVRAFGAGLLPPLYSLVFIIGVGVNVLVILVLMQHRRLQSMTSIY 72

Qy      81 LLNLAISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTIDRY 139
      | |||:|:|:| ||| | : :|:|:|:| ||| :| |:| : ||||| |||
Db      73 LFNLAVSDLVFLFTLPFWIDYKLKDDWIFGDAMCKLLSGFYILGLYSEIFFIILLTIDRY 132

Qy     140 LAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---- 195
      ||||| |||:| ||| |:|:|:| |:| |:| : | | | : | |:|
Db     133 LAIVHAVFALRARTVTLGIITSIITWALAILASMPALYFFKAQWEFTHRTCSPHFPYKSL 192

Qy     196 RGWNNFHTIMRNILGLVLPLLLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLF 255
      : | | : |:|:|:|:|:|:|:|:|:|:| | | |:|:|:| | :|:|
Db     193 KQWKRFQALKLNLGLLPLLVMIICYAGIIRILLR-RPSEKKVKAVRLIFAITLLFFLL 251

Qy     256 WTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF--- 312
      ||||: : :| |: : || : || | ||| : |||:| ||| |||:|
Db     252 WTPYNLSVFVSAFQDVLFTNQCEQSKHLDLAMQVTEVIAYTHCCVNPIIYFVGERFWKY 311

Qy     313 -RSLF--HIALGCRIAPLQK 329
      | || |:|: || |
Db     312 LRQLFQRHVAI-----PLAK 326

```

# RESULT 7

G02436

chemokine (C-C) receptor 3 - human

N;Alternate names: C-C CKR-3

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004

C;Accession: G02436; A57237

R;Ponath, P.D.

submitted to the EMBL Data Library, February 1996

A;Reference number: H01272

A;Accession: G02436

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-355 <PON>

A;Cross-references: UNIPROT:P51677; EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477561

R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.

J. Biol. Chem. 270, 16491-16494, 1995

A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.

A;Reference number: A57237; MUID:95348056; PMID:7622448

A;Accession: A57237

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>

A;Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580

A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.1, differs from the published sequence in having 281-Leu  
 C;Genetics:  
 A;Gene: GDB:CMKBR3  
 A;Cross-references: GDB:579624; OMIM:601268  
 A;Map position: 3p21-3p21  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein  
 F;36-60/Domain: transmembrane #status predicted <TM1>  
 F;71-91/Domain: transmembrane #status predicted <TM2>  
 F;108-129/Domain: transmembrane #status predicted <TM3>  
 F;147-171/Domain: transmembrane #status predicted <TM4>  
 F;205-223/Domain: transmembrane #status predicted <TM5>  
 F;240-261/Domain: transmembrane #status predicted <TM6>  
 F;288-305/Domain: transmembrane #status predicted <TM7>  
 F;24-273,106-183/Disulfide bonds: #status predicted  
 F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 45.2%; Score 890.5; DB 2; Length 355;  
 Best Local Similarity 54.6%; Pred. No. 2.7e-70;  
 Matches 167; Conservative 56; Mismatches 72; Indels 11; Gaps 5;

Qy	21	TTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIY	80
		:::        : :   :            : :::        : :	
Db	14	TSYYD-DVGLLCEKADTRALMAQFVPPPLYSLVFTVGLLGNVVVMILIKYRRRLRIMTNIY	72
Qy	81	LLNLAISDLLFLITLPLWAHSA-ANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRY	139
		:      :       :       :       :	
Db	73	LLNLAISDLLFLVTLPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRY	132
Qy	140	LAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR---	196
		:          : :      :    : : :   :	
Db	133	LAIVHAVFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEETLCSALYPEDTV	192
Qy	197	-GWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLF	255
		:    :         :      :      :     : :      : :	
Db	193	YSWRHFHTLRMTIFCLVLP LLVMAICYTGIIKTLLRCPS-KKKYKAIRLIFVIMAVFFIF	251
Qy	256	WTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRS-	314
		:     : :  : :        :     :       :	
Db	252	WTPYNVAILLSSYQSILFGNDCERTKHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKY	311
Qy	315	---LFH	317
Db	312	LRHFFH	317

# RESULT 8

JC4587

chemokine (C-C) receptor 4 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 08-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004

C;Accession: JC4587

R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.  
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996

A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human CC CKR-4.  
A;Reference number: JC4587; MUID:96136324; PMID:8573157  
A;Accession: JC4587  
A;Molecule type: mRNA  
A;Residues: 1-360 <HOO>  
A;Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852  
A;Experimental source: thymus  
C;Genetics:  
A;Gene: cc ckr-4  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: glycoprotein; phosphoprotein; receptor; thymus  
F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted  
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 42.3%; Score 833; DB 2; Length 360;  
Best Local Similarity 47.9%; Pred. No. 2.9e-65;  
Matches 160; Conservative 63; Mismatches 89; Indels 22; Gaps 5;

```

Qy      10 IRNTNESGEEVTTFDDYD-YGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILI 68
      : : | :      : : : | :      | | | : | | | | | | | : | | | : | | : |
Db      6 VDTTQDET VYNSYFYFESMPKPCTKEGIKAFGEVFLPPLYSLVFLGLGFGNSVVVLVLF 65

Qy      69 NCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGI 128
      | : | | : | : | | | | | | | | : : | | : | : | | | : | : | : | |
Db      66 KYKRLKSMTDVYLLNLAISDLLFVLSLPFWGYAADQWVFGGLCKIVSWMYLVGFYSGI 125

Qy     129 FFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVY 188
      | | : | : : | | | | | | | | : | | : | | : | | | | : | | : | : |
Db     126 FFIMLSIDRYLAIVHAVFSLKARTLTGYVITSLITWSVAVFASLPGLLFSTCYTEHNHT 185

Qy     189 VCGPYF---PRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHRVRVI 245
      | :      |      : : | : | : : | | : | | | : : | | : | | | : | | : |
Db     186 YCKTQYSVNSTTWKVLSSLEINVLGLLIPLGIMLFWYSMIIRTLOHCKNEKK-NRAVRMI 244

Qy     246 FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIY 305
      | : : : : | | | | : | : | | | : | | | | | | | | | | | : | | : |
Db     245 FGVVVLFLGFWTPYNVVLFLETLVELEVLQDCTLERYLDYAIQATETLGFHCCCLNPVIY 304

Qy     306 AFVGEKFR----SLFHIALGCRIAPLQKPVCGGP 335
      | : | | | |      | |      | |
Db     305 FFLGEKFRKYITQLFR-----TCRGP 325

```

# RESULT 9

A57160

chemokine (C-C) receptor 4 - human

N;Alternate names: C-C CKR-4

C;Species: Homo sapiens (man)

C;Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C;Accession: A57160

R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; Wells, T.N.C.  
 J. Biol. Chem. 270, 19495-19500, 1995  
 A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line.  
 A;Reference number: A57160; MUID:95370289; PMID:7642634  
 A;Accession: A57160  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-360 <POW>  
 A;Cross-references: UNIPROT:P51679; GB:X85740; NID:gl370103; PIDN:CAA59743.1; PID:g971452  
 A;Note: source clone K5-5  
 C;Genetics:  
 A;Gene: GDB:CMKBR4  
 A;Cross-references: GDB:677463  
 A;Map position: 3p21-3p21  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein  
 F;40-65/Domain: transmembrane #status predicted <TM1>  
 F;76-97/Domain: transmembrane #status predicted <TM2>  
 F;112-133/Domain: transmembrane #status predicted <TM3>  
 F;151-175/Domain: transmembrane #status predicted <TM4>  
 F;208-226/Domain: transmembrane #status predicted <TM5>  
 F;243-264/Domain: transmembrane #status predicted <TM6>  
 F;291-308/Domain: transmembrane #status predicted <TM7>  
 F;29-276,110-187/Disulfide bonds: #status predicted  
 F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted  
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
 F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 42.2%; Score 831.5; DB 2; Length 360;  
 Best Local Similarity 51.9%; Pred. No. 3.9e-65;  
 Matches 154; Conservative 58; Mismatches 80; Indels 5; Gaps 3;

Qy	31	PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAISDLL	90
		:                 :     :     :     :     :	
Db	28	PCTKEGIKAFGELFLPPLYSLVFVFGLLGNSVVVLVLFKYKRLRSMTDVYLLNLAISDLL	87
Qy	91	FLITLPLWAHSAANEVVFNGAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVHAVFALK	150
		: :     :   : :       :   : : :   : : :     : : :                 : :	
Db	88	FVFSLPFWGYAADQWVFGGLCKMISWMYLVGFYSGIFFVMLMSIDRYLAIVHAVFSLR	147
Qy	151	ARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---WNNFHTIMRN	207
		:   :   :   :             :   :     :     :     :     :	
Db	148	ARTLTYGVITSLATWSVAVFASLPGFLFSTCYTERNHTYCKTKYSLNSTTWKVLSSLEIN	207
Qy	208	ILGLVLP LLIMVICYSGILKTLRLCRNEKKRRAVRVIFTIMIVYFLFWTPYNIVILLNT	267
		:       :       : :       :       :     : : :           :	
Db	208	ILGLVIPLGIMLFCYSMIIRTLQHCNEKK-NKAVKMIFAVVVLFLGFWTPYNIVLFLET	266
Qy	268	FQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRS-LFHIALGCR	323



Db 267 LVELEVLQDCTFERYLDAIQATETLAFVHCCLNPIIYFFLGEKFRKYILQLFKTCR 323

RESULT 10

S55594

G protein-coupled receptor E1 - equine herpesvirus 2

C;Species: equine herpesvirus 2

C;Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004

C;Accession: S55594

R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.

J. Mol. Biol. 249, 520-528, 1995

A;Title: The DNA sequence of equine herpesvirus 2.

A;Reference number: S55594; MUID:95302501; PMID:7783207

A;Accession: S55594

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-383 <TEL>

A;Cross-references: UNIPROT:Q89609; GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 40.3%; Score 794.5; DB 2; Length 383;  
Best Local Similarity 44.3%; Pred. No. 7.2e-62;  
Matches 164; Conservative 60; Mismatches 107; Indels 39; Gaps 7;

Qy 4 TSRSRFIRNTNESGEEVTTFFDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNM 61  
| : : : : | | : | | | | : : | : : | | | : : | : :  
Db 32 TTIASLVPSTNSSEDYYDDLDDVDYEEAPCYKSDTTRLAAQVVPALYLLVFLFGLLGN 91  
  
Qy 62 LVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAH--SAANEWVFGNAMCKLFTGL 119  
| | : : | : | | : : | | | | | | : | | : : | : : | :  
Db 92 LVVIIVIRYMKIKNLTNMLLLNLAISDLLFLTLPLPFWMHYIGMYHDWTFGISLCKLLRGV 151  
  
Qy 120 YHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFT 179  
: : : : | | | : : | : : | : : | : : | : : | : : | : :  
Db 152 CYMSLYSQVFCIILLTVDRYLAVVYAVTALRFRTVTCGIVTCVCTWFLAGLLSLPEFFFH 211  
  
Qy 180 KCQKEDSVYVCGPYFP----RGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNE 235  
| : : | | : : | | : : | : : | : : | : : | : : | : :  
Db 212 GHQDDNGRVQCDPYPEMSTNVWRRRAHVAKVIMLSLILPLLIMAVCYVIIRLLR-RPS 270  
  
Qy 236 KKRHRARVVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGM 295  
| : : : : | : : | : : | : : | : : | : : | : : | : : | : :  
Db 271 KKKYKAIRLIFVIMVAYFVFWTPYNIVLLLSTFHATLLNLQCALSSNLDMALLITKT VAY 330  
  
Qy 296 THCCINPIIYAFVGEKFR----SLFHIALG---CRIAPLQKPVCGGPGVRPGKNVKVTTQ 348  
| | | | : : | | | | | : : | : : | : : | : : | : :  
Db 331 THCCINPVIYAFVGEKFRRLHYHFFHTYVAIYLCKYIP----- 368  
  
Qy 349 GLLDGRGKGK 358  
| | | : : |  
Db 369 -FLSGDGEGK 377

RESULT 11

I49340

MIP-1 alpha receptor like-1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: I49340

R;Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.

A;Reference number: I49339; MUID:95340546; PMID:7542241

A;Accession: I49340

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-356 <RES>

A;Cross-references: UNIPROT:P51676; EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550

C;Superfamily: vertebrate rhodopsin

Query Match 37.1%; Score 731; DB 2; Length 356;  
Best Local Similarity 46.6%; Pred. No. 2.4e-56;  
Matches 137; Conservative 59; Mismatches 92; Indels 6; Gaps 3;

```
Qy      25 DYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNL 84
      |: | | :|: | : | | | | | | | | :|:| | | | | | | | | | |
Db      18 DFMSGFLCFSINVRAFGITVPTPLYSLVFIIGVIGHVLVVLVLIQHKRLRNMTSIYLFNL 77

Qy      85 AISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIV 143
      | | | | :| | | | : : | | | | | | | | :| | | | | | | | | |
Db      78 AISDLVFLSTLPFWVDYIMKGDWIFGNAMCKFVSGFYFYLGLYSDFITLLTIDRYLAVV 137

Qy     144 HAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR----GWN 199
      | | | | :| | | | | :| | | | | | | | | | :| | | | | | |
Db     138 HVVFALRARTVTFGIISIIITWVLAALVSIPCLYVFKSQMEFTYHTCRAILPRKSLIRFL 197

Qy     200 NFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVAVRVIFTIMIVYFLFWTPY 259
      | : | | | | :| | | | | :| | | | | | | | | | :| | | | |
Db     198 RFQALTMNIGLILPLLAMIICYTRIINVLRH-RPNKKKAKVMRLIFVITLLFFLLAPY 256

Qy     260 NIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR 313
      : : | : | : | : | : | : | | | | | | | | | | | | |
Db     257 YLAAFVSAFEDVLFTPSCLRSQQVDLSLMITEALAYTHCCVNPVIYVFVGKRFR 310
```

RESULT 12

JC5067

G protein-coupled receptor CKR-L1 - human

N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 09-Jul-2004

C;Accession: JC5067; G02776; G02387

R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like genes.

A;Reference number: JC5067; MUID:97040707; PMID:8886020

A;Accession: JC5067

A;Molecule type: DNA  
A;Residues: 1-355 <ZAB>  
A;Cross-references: UNIPROT:P51685; EMBL:Z79782; NID:g1668735; PIDN:CAB02142.1; PID:g1668736  
R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.  
submitted to the EMBL Data Library, June 1996  
A;Reference number: H01714  
A;Accession: G02776  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-355 <NAP>  
A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979  
R;Bonner, T.I.  
submitted to the EMBL Data Library, January 1996  
A;Reference number: H01154  
A;Accession: G02387  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-355 <BON>  
A;Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057  
C;Comment: This protein belongs to the family of beta chemokine receptors.  
C;Genetics:  
A;Gene: GDB:CMKBR8; CMKBRL2; TER1; CKR-L1  
A;Cross-references: GDB:6053733; OMIM:601834  
A;Map position: 3p21-3p21  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; transmembrane protein  
F;36-63/Domain: transmembrane #status predicted <TM1>  
F;73-94/Domain: transmembrane #status predicted <TM2>  
F;108-129/Domain: transmembrane #status predicted <TM3>  
F;147-171/Domain: transmembrane #status predicted <TM4>  
F;200-222/Domain: transmembrane #status predicted <TM5>  
F;239-260/Domain: transmembrane #status predicted <TM6>  
F;281-304/Domain: transmembrane #status predicted <TM7>

Query Match 36.7%; Score 723; DB 2; Length 355;  
Best Local Similarity 43.5%; Pred. No. 1.2e-55;  
Matches 131; Conservative 59; Mismatches 103; Indels 8; Gaps 3;

Qy	20	VTTFDYDY----	GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKC	75
			:   ::        :    :     : :  :   :	
Db	9	VTTVTDYYPDIFSSPCDAELIQTNGKLLAVFYCLLFVFSLLGNSLVILVLVCKKLRS	68	
Qy	76	LTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFFIILLT	135	
		:  :     :    :   :	:       :   :   : :    : :	
Db	69	ITDVYLLNLALSDLLFVFSFPFQTYLLDQWVFGTVMCKVVSGFYIIGFYSSMFFITLMS	128	
Qy	136	IDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP	195	
		:    :    :       :	:     :   :        : :	
Db	129	VDRYLAVVHAVYALKVRTIRMGTTLC LAVWLTAIMATIPLLVFYQVASEDGVLCQCYSFYN	188	
Qy	196	R---GWNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHRVAVRVIIFTIMIVY	252	
		:	:    :           :    :  : : : :	
Db	189	QOTLKWKIFTNFKMNILGLLPFTIFMFCYIKILHQLKRCQNHNKT-KAIRLVLVIVIAS	247	
Qy	253	FLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF	312	

```

      ||| |:|:|: | :      | | : || || ||| : |||:|:| |||||
Db      248 LLFWVPFNVVLFSLHSMHILDGCSISQQLTYATHVTEIISFTHCCVNPVIYAFVGEKF 307

Qy      313 R 313
      :
Db      308 K 308

```

RESULT 13

I58186

probable G protein-coupled receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004

C;Accession: I58186

R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.

Neurosci. Lett. 169, 85-89, 1994

A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and brain related to chemokine receptors.

A;Reference number: I58186; MUID:94323113; PMID:8047298

A;Accession: I58186

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-354 <RES>

A;Cross-references: UNIPROT:P35411; EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 35.8%; Score 704.5; DB 2; Length 354;

Best Local Similarity 47.6%; Pred. No. 5e-54;

Matches 151; Conservative 43; Mismatches 112; Indels 11; Gaps 6;

```

Qy      24 FDYDYG-PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLL 82
      |:| | |: | | |||| | ||:| | | :| | :| | |
Db      13 FEYDDSAEACYLGDIVAFGTIFLSIFYSLVFTFGLVGNLLVVLALTNSRKSITSITDIYLL 72

Qy      83 NLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAI 142
      |||:| | |: | | : |||| | : |:| | | | :::| | | |
Db      73 NLALSDLLFVATLPFWTHYLISHEGLHNAMCKLTTAFFFIGFFGGIFFITVISIDRYLAI 132

Qy      143 VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRGWNNFH 202
      | | :: | | | | |: | | : | :| | :|: | | :|
Db      133 VLAANSMMNRTVQHGVTTISLGVWAAAILVASPQFMFTK-RKDNE---CLGDYPEVLQEIW 188

Qy      203 TIMR---NILGLVLP LLIMVICYS GILKTL LRCRNEKKRHRAVRVIFTIMIVYFLFWTP 258
      ::| ||| | | | | | | | | |:| | |:| | | |:|:| :::|:| | | |
Db      189 PVLNRNSEVNILGFVLP LLIMSF CYFRIVRTLFSCKNRKKA-RAIRLILLVVVVFFLEFWTP 247

Qy      259 YNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRS-LFH 317
      |||| | | : : | | | | | | | | |:|:| | | | | | | |
Db      248 YNIVIFLET LKFYNFFPSCGMKRD LRWALSVTETVAFSHCCLNPF IYAFAGEKFRRYLRH 307

Qy      318 IALGCRIAPLQKPVC GG 334
      : | :| |
Db      308 LYNKCLAVLCGRPVHAG 324

```

RESULT 14

JC4304

orphan G protein-coupled receptor - human

N;Alternate names: V28 protein

C;Species: Homo sapiens (man)

C;Date: 16-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004

C;Accession: JC4304

R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.  
Gene 163, 295-299, 1995

A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to genes for chemokine receptors and is expressed in lymphoid and neuraltissues.

A;Reference number: JC4304; MUID:96011651; PMID:7590284

A;Accession: JC4304

A;Molecule type: mRNA

A;Residues: 1-355 <RAP>

A;Cross-references: UNIPROT:P49238; GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581

A;Experimental source: peripheral blood mononuclear cell

C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals and transduces those signals into an intracellular response.

C;Comment: This protein is a key regulator of many immune and homeostatic responses, and interacts between the nervous and immune systems.

C;Genetics:

A;Gene: v28

A;Map position: 3pter-p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein

F;35-57/Domain: transmembrane #status predicted <TM1>

F;66-88/Domain: transmembrane #status predicted <TM2>

F;104-125/Domain: transmembrane #status predicted <TM3>

F;146-165/Domain: transmembrane #status predicted <TM4>

F;197-217/Domain: transmembrane #status predicted <TM5>

F;230-254/Domain: transmembrane #status predicted <TM6>

F;275-296/Domain: transmembrane #status predicted <TM7>

Query Match 35.4%; Score 698; DB 2; Length 355;

Best Local Similarity 45.3%; Pred. No. 1.9e-53;

Matches 146; Conservative 49; Mismatches 111; Indels 16; Gaps 7;

```

Qy      18  EEVTTFFDY-DYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCL 76
          |||  |:|  |  |:  |:  |  |  ||::|  |  ||:||||  |  |||  |  :
Db      6  ESVTENFEYDDLAEACYIGDIVVFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSV 65

Qy      77  TDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFFIILLTI 136
          |||||:||||: |||  |  ||  ||||  |  :  ||:|  ||||  ::|
Db      66  TDIYLLNLALSDLLFVATLPFWTHYLINEKGLHNAMCKFTTAAFFFIGFFGSIFFITVISI 125

Qy     137  DRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKQKEDSVYVCGPYFPR 196
          |||||  |  ::  |||  ||  |:  |  |:  :  |  |||  |||:  |  :|
Db     126  DRYLAIVLAANSMMNRTVQHGVTISLGVWAAAILVAAPQFMFTK-QKENE---CLGDYPE 181

Qy     197  GWNNFHTIMRNI----LGLVLP LLIMVICYSGILKTL LRCRNEKKRHRAVRVI FTIMIVY 252
          ::||:  ||  :||||  ||  |:||  |:|  ||  ::::|  ::||:
Db     182  VLQEIWPVLRNVETNFLGFLPL LIMSICYFRIIQTLFSCKNHKKA-KAIKLILLVVIVF 240

```

Qy 253 FLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF 312  
 |||||:::| | : : :|: | | |||: :||:|:|||| ||||  
 Db 241 FLFWTPYNVMIFLETCLKLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKF 300  
 Qy 313 RS-LFHIALGCRIAPLQKPVCVCG 333  
 | |:|: | :||  
 Db 301 RRYLYHLYGKCLAV-----LCG 317

# RESULT 15

JC5942

chemokine receptor - human

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: JC5942

R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.

Biochem. Biophys. Res. Commun. 243, 264-268, 1998

A;Title: Cloning and characterization of a novel human chemokine receptor.

A;Reference number: JC5942; MUID:98139902; PMID:9473515

A;Accession: JC5942

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-344 <FAN>

A;Cross-references: UNIPROT:O00421; GB:U97123; NID:g2897070; PIDN:AAC39595.1;

PID:g2897071

C;Superfamily: vertebrate rhodopsin

Query Match 32.7%; Score 644.5; DB 2; Length 344;  
 Best Local Similarity 39.9%; Pred. No. 8.7e-49;  
 Matches 132; Conservative 58; Mismatches 120; Indels 21; Gaps 6;

Qy 27 DYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAI 86  
 | | |:| : : ||:| | | ||: | : |:|||||: | | : :|||||:  
 Db 23 DEAEQCDKYDAQALSAQLVPSLCSAVFVIGVLDNLLVVLILVKYKGLKRVENIYLLNLAV 82  
 Qy 87 SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVH-A 145  
 |:| ||:|||| |:| : |||: ||| :| : || |||: ||| :|  
 Db 83 SNLCFLLTLPLFWAHAG-----GDPMCKILIGLYFVGLYSETFFNCLLTVQRYLVFLHKG 136  
 Qy 146 VFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCG----PYFPRG---W 198  
 | | |:||||: |: |: |:| : | | | | | | |: | |  
 Db 137 NFFSARRRVPCGIITSVLAWVTAILATLPEYVVYKQMEDQKYKCAFSRTPFLPADETFW 196  
 Qy 199 NNFHTIMRNILGLVLP LLIMVICYS GILKTL LRCRNEKKRHRVRVIFTIMIVYFLFWTP 258  
 :| |: || ||||| | : ||| | :||: :||: ||:| |||:  
 Db 197 KHFLT LKMNISVLVLP LFIFTFLYVQMRKTL---RFREQRYSLFKLVFAIMVVFLMWAP 253  
 Qy 259 YNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRS---- 314  
 ||| |:|:| | ||:|:| |:| :|: : | |||||:|:|:| |  
 Db 254 YNIAFFLSTFKEHFSLS DCKSSYNLDKSVHITKLIATTHCCINPLLYAFLDGTF SKYLCR 313  
 Qy 315 LFHIALGCRIAPLQKPVCVCGGPGVRPGKNVKV 345  
 ||: : | : | : | :|  
 Db 314 CFHLRSNTPLQPRGQSAQGTSREEPDHSTEV 344

Search completed: January 10, 2005, 11:35:10

Job time : 41 secs

OM protein - protein search, using sw model

Run on: January 10, 2005, 11:33:45 ; Search time 750 Seconds  
(without alignments)  
179.805 Million cell updates/sec

Title: US-10-791-592-2  
Perfect score: 1970  
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES



Result No.	Score	Query Match	Length	DB	ID	Description
1	1970	100.0	374	10	US-09-893-512-13	Sequence 13, Appl
2	1970	100.0	374	14	US-10-039-659-14	Sequence 14, Appl
3	1970	100.0	374	14	US-10-239-423-63	Sequence 63, Appl
4	1970	100.0	374	16	US-10-754-071-14	Sequence 14, Appl
5	1970	100.0	374	16	US-10-741-601-287	Sequence 287, App
6	1970	100.0	374	17	US-10-791-592-2	Sequence 2, Appli
7	1970	100.0	374	17	US-10-791-166-2	Sequence 2, Appli
8	1823	92.5	344	9	US-09-779-879A-9	Sequence 9, Appli
9	1823	92.5	344	9	US-09-779-880A-9	Sequence 9, Appli
10	1823	92.5	344	14	US-10-232-686-9	Sequence 9, Appli
11	1823	92.5	344	14	US-10-067-800-9	Sequence 9, Appli
12	1823	92.5	344	14	US-10-135-839-9	Sequence 9, Appli
13	1727.5	87.7	329	9	US-09-725-285-9	Sequence 9, Appli
14	1727.5	87.7	329	9	US-09-195-662A-9	Sequence 9, Appli
15	1727.5	87.7	329	9	US-09-339-912A-9	Sequence 9, Appli
16	1727.5	87.7	329	9	US-09-502-783A-9	Sequence 9, Appli
17	1727.5	87.7	329	16	US-10-791-905-9	Sequence 9, Appli
18	1651.5	83.8	360	9	US-09-131-827A-2	Sequence 2, Appli
19	1651.5	83.8	360	14	US-10-225-567A-460	Sequence 460, App
20	1651.5	83.8	360	14	US-10-164-649-50	Sequence 50, Appl
21	1651.5	83.8	360	14	US-10-239-423-64	Sequence 64, Appl
22	1651.5	83.8	360	14	US-10-439-845-8	Sequence 8, Appli
23	1651.5	83.8	360	16	US-10-741-601-285	Sequence 285, App
24	1651.5	83.8	360	16	US-10-741-601-286	Sequence 286, App
25	1651.5	83.8	360	17	US-10-791-592-4	Sequence 4, Appli
26	1651.5	83.8	360	17	US-10-791-166-4	Sequence 4, Appli
27	1651.5	83.8	360	17	US-10-700-313-8	Sequence 8, Appli
28	1650.5	83.8	360	9	US-09-131-827A-20	Sequence 20, Appl
29	1645.5	83.5	360	9	US-09-938-719-7	Sequence 7, Appli
30	1645.5	83.5	360	9	US-09-939-226-7	Sequence 7, Appli
31	1645.5	83.5	360	9	US-09-938-703-7	Sequence 7, Appli
32	1645.5	83.5	360	10	US-09-826-509-473	Sequence 473, App
33	1645.5	83.5	360	16	US-10-661-798-7	Sequence 7, Appli
34	1645.5	83.5	360	16	US-10-612-791-7	Sequence 7, Appli
35	1614.5	82.0	360	14	US-10-164-649-51	Sequence 51, Appl
36	1589.5	80.7	347	9	US-09-104-792-3	Sequence 3, Appli
37	1589.5	80.7	347	14	US-10-176-078-3	Sequence 3, Appli
38	1589.5	80.7	347	17	US-10-893-996-3	Sequence 3, Appli
39	1582.5	80.3	384	10	US-09-893-512-14	Sequence 14, Appl
40	1236	62.7	352	14	US-10-151-274-5	Sequence 5, Appli
41	1230	62.4	352	14	US-10-164-649-52	Sequence 52, Appl
42	1224	62.1	352	9	US-09-725-285-2	Sequence 2, Appli
43	1224	62.1	352	9	US-09-759-841-2	Sequence 2, Appli
44	1224	62.1	352	9	US-09-779-879A-22	Sequence 22, Appl
45	1224	62.1	352	9	US-09-779-880A-22	Sequence 22, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-893-512-13

; Sequence 13, Application US/09893512

; Publication No. US20030017530A1

```

; GENERAL INFORMATION:
; APPLICANT: OWMAN, CHRISTER
; TITLE OF INVENTION: HEPTAHELIX RECEPTOR AND ITS USE AS LEUKOTRIENE B4
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 07675.0001-03 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/09/893,512
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/061,789
; PRIOR FILING DATE: 1997-10-14
; PRIOR APPLICATION NUMBER: 60/081,958
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 09/170,069
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-512-13

```

```

Query Match          100.0%; Score 1970; DB 10; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRLSFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRLSFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
        ||||||||||||||||
Db    361 GRAPEASLQDKEGA 374

```

```

RESULT 2
US-10-039-659-14
; Sequence 14, Application US/10039659

```

```

; Publication No. US20030018167A1
;   GENERAL INFORMATION:
;       APPLICANT: Wang, Wei
;               Gish, Kurt C.
;               Schall, Thomas J.
;               Vicari, Alain P.
;               Zlotnik, Albert
;   TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: DNAX Research Institute
;       STREET: 901 California Avenue
;       CITY: Palo Alto
;       STATE: California
;       COUNTRY: USA
;       ZIP: 94304-1104
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/039,659
;       FILING DATE: 03-Jan-2002
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 08/887,977
;       FILING DATE: 03-JUL-1997
;       APPLICATION NUMBER: US 60/021,644
;       FILING DATE: 05-JUL-1996
;       APPLICATION NUMBER: US 60/028,329
;       FILING DATE: 11-OCT-1996
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Ching, Edwin P.
;       REGISTRATION NUMBER: 34,090
;       REFERENCE/DOCKET NUMBER: DX0589K1
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 650-852-9192
;       TELEFAX: 650-496-1200
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 374 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-039-659-14

```

```

Query Match          100.0%;  Score 1970;  DB 14;  Length 374;
Best Local Similarity 100.0%;  Pred. No. 3.4e-163;
Matches 374;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

```

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120  
 |||  
 Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 |||  
 Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240  
 |||  
 Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300  
 |||  
 Db 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360  
 |||  
 Db 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy 361 GRAPEASLQDKEGA 374  
 |||  
 Db 361 GRAPEASLQDKEGA 374

# RESULT 3

US-10-239-423-63

; Sequence 63, Application US/10239423

; Publication No. US20030186889A1

; GENERAL INFORMATION:

; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;

; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj

; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the

; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells  
 and

; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,

; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine

; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand

Interaction

; FILE REFERENCE: 022217us

; CURRENT APPLICATION NUMBER: US/10/239,423

; CURRENT FILING DATE: 2002-09-23

; PRIOR APPLICATION NUMBER: DE10016013.1

; PRIOR FILING DATE: 2000-03-31

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 63

; LENGTH: 374

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies

US-10-239-423-63

Query Match 100.0%; Score 1970; DB 14; Length 374;

Best Local Similarity 100.0%; Pred. No. 3.4e-163;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
      ||||||||||||||
Db    361 GRAPEASLQDKEGA 374

```

RESULT 4

US-10-754-071-14

```

; Sequence 14, Application US/10754071
; Publication No. US20040137578A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Schall, Thomas J.
; APPLICANT: Vicari, Alain P.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Chemokine TECK Polypeptides
; FILE REFERENCE: DX0589K1C US
; CURRENT APPLICATION NUMBER: US/10/754,071
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 10/039,659
; PRIOR FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1

```

; SEQ ID NO 14  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-754-071-14

Query Match 100.0%; Score 1970; DB 16; Length 374;  
Best Local Similarity 100.0%; Pred. No. 3.4e-163;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
        ||||||||||||
Db    361 GRAPEASLQDKEGA 374
```

RESULT 5

US-10-741-601-287

; Sequence 287, Application US/10741601  
; Publication No. US20040166519A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001500  
; CURRENT APPLICATION NUMBER: US/10/741,601  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 26415  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 287  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-741-601-287

Query Match 100.0%; Score 1970; DB 16; Length 374;  
Best Local Similarity 100.0%; Pred. No. 3.4e-163;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
        ||||||||||||
Db    361 GRAPEASLQDKEGA 374
```

RESULT 6

US-10-791-592-2

; Sequence 2, Application US/10791592

; Publication No. US20040219644A1

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

```

;      APPLICATION NUMBER: US/10/791,592
;      FILING DATE: 01-Mar-2004
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/09/625,573
;      FILING DATE: 25-Jul-2000
;      APPLICATION NUMBER: US/08/446,669
;      FILING DATE: May 25, 1995
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Neeley, Richard
;      REGISTRATION NUMBER: 30,092
;      REFERENCE/DOCKET NUMBER: UCAL-237/01US
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 415-843-5000
;      TELEFAX: 415-857-0663
;      TELEX: 380816CooleyPA
;      INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 374 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-791-592-2

```

```

Query Match          100.0%;  Score 1970;  DB 17;  Length 374;
Best Local Similarity 100.0%;  Pred. No. 3.4e-163;
Matches 374;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
        ||||||||||||
Db    361 GRAPEASLQDKEGA 374

```





```

Qy      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy     121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy     181 CQKEDSVYVCGPYFPRGWNNFHTIMRNLGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CQKEDSVYVCGPYFPRGWNNFHTIMRNLGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy     241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy     301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy     361 GRAPEASLQDKEGA 374
        ||||||||||||
Db     361 GRAPEASLQDKEGA 374

```

RESULT 8

US-09-779-879A-9

```

; Sequence 9, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDG NR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-09-779-879A-9

```

Query Match          92.5%; Score 1823; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 2e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77

```

Db	1	EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT	60
Qy	78	DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID	137
Db	61	DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID	120
Qy	138	RYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	197
Db	121	RYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	180
Qy	198	WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT	257
Db	181	WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT	240
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	317
Db	241	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	300
Qy	318	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG	361
Db	301	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG	344

RESULT 9

US-09-779-880A-9

; Sequence 9, Application US/09779880A

; Patent No. US20020061834A1

; GENERAL INFORMATION:

; APPLICANT: Rosen, Craig A.

; APPLICANT: Roschke, Viktor

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven, M.

; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10

; FILE REFERENCE: 1488.115000C

; CURRENT APPLICATION NUMBER: US/09/779,880A

; CURRENT FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: US 60/181,258

; PRIOR FILING DATE: 2000-02-09

; PRIOR APPLICATION NUMBER: US 60/187,999

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: US 60/234,336

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9

; LENGTH: 344

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-779-880A-9

Query Match 92.5%; Score 1823; DB 9; Length 344;

Best Local Similarity 100.0%; Pred. No. 2e-150;

Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	18	EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT	77

Db 1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 137  
 |||

Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 120

Qy 138 RYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197  
 |||

Db 121 RYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy 198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257  
 |||

Db 181 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240

Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317  
 |||

Db 241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300

Qy 318 IALGCRIAPLQKPVCGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361  
 |||

Db 301 IALGCRIAPLQKPVCGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344

RESULT 10

US-10-232-686-9

; Sequence 9, Application US/10232686  
 ; Publication No. US20030023044A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Yi  
 ; APPLICANT: Ruben, Steven M.  
 ; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10  
 ; FILE REFERENCE: 1488.115000N  
 ; CURRENT APPLICATION NUMBER: US/10/232,686  
 ; CURRENT FILING DATE: 2002-09-03  
 ; PRIOR APPLICATION NUMBER: 09/339,912  
 ; PRIOR FILING DATE: 1999-06-25  
 ; PRIOR APPLICATION NUMBER: 09/195,662  
 ; PRIOR FILING DATE: 1998-11-18  
 ; PRIOR APPLICATION NUMBER: 08/466,343  
 ; PRIOR FILING DATE: 1995-06-06  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 344  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-10-232-686-9

Query Match 92.5%; Score 1823; DB 14; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 2e-150;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77  
 |||

Db 1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 137



```

Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKCLKLT 60
Qy          78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 137
Db          61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 120
Qy          138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
Db          121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180
Qy          198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 257
Db          181 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 240
Qy          258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
Db          241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300
Qy          318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
Db          301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344

```

RESULT 12

US-10-135-839-9

```

; Sequence 9, Application US/10135839
; Publication No. US20030166024A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDG NR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/10/135,839
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-839-9

```

```

Query Match          92.5%; Score 1823; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 2e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy          18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKCLKLT 77

```

```

Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT  60
Qy          78 DIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
            |||
Db          61 DIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120
Qy          138 RYLAIVHAVFALKARTVTFGVVT SVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
            |||
Db          121 RYLAIVHAVFALKARTVTFGVVT SVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180
Qy          198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVAVRVI FTIMIVYFLFWT 257
            |||
Db          181 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVAVRVI FTIMIVYFLFWT 240
Qy          258 PYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
            |||
Db          241 PYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300
Qy          318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
            |||
Db          301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344

```

RESULT 13

US-09-725-285-9

; Sequence 9, Application US/09725285

; Patent No. US20010000241A1

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven, M.

; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10

; TITLE OF INVENTION: (CCR5 Receptor)

; FILE REFERENCE: 1488.1150003

; CURRENT APPLICATION NUMBER: US/09/725,285

; CURRENT FILING DATE: 2000-11-29

; PRIOR APPLICATION NUMBER: 09/339,912

; PRIOR FILING DATE: 1999-06-25

; PRIOR APPLICATION NUMBER: 09/195,662

; PRIOR FILING DATE: 1998-11-18

; PRIOR APPLICATION NUMBER: 08/466,343

; PRIOR FILING DATE: 1995-06-06

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9

; LENGTH: 329

; TYPE: PRT

; ORGANISM: Protein

US-09-725-285-9

Query Match 87.7%; Score 1727.5; DB 9; Length 329;

Best Local Similarity 95.6%; Pred. No. 3.9e-142;

Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

```

Qy          18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT  77
            |||
Db          1  EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT  60

```

Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 137  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105

Qy 138 RYLAIHVHAFALKARTVTFGVVTSVITWLAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 106 RYLAIHVHAFALKARTVTFGVVTSVITWLAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy 198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 166 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225

Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy 318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329

RESULT 14

US-09-195-662A-9

; Sequence 9, Application US/09195662A

; Patent No. US20020076745A1

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven, M.

; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDG NR10 (CCR5 Receptor)

; FILE REFERENCE: 1488.1150002

; CURRENT APPLICATION NUMBER: US/09/195,662A

; CURRENT FILING DATE: 1998-11-18

; PRIOR APPLICATION NUMBER: 08/466,343

; PRIOR FILING DATE: 1995-06-06

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9

; LENGTH: 329

; TYPE: PRT

; ORGANISM: Protein

US-09-195-662A-9

Query Match 87.7%; Score 1727.5; DB 9; Length 329;

Best Local Similarity 95.6%; Pred. No. 3.9e-142;

Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

Qy 18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 137  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105

Qy 138 RYLAIHVHAFALKARTVTFGVVTSVITWLAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197



```

Db      106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165
Qy      198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
Db      166 WNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHRAVRVIFTIMIVYFLFWT 225
Qy      258 PYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
Db      226 PYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285
Qy      318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
Db      286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329

```

RESULT 15

US-09-339-912A-9

; Sequence 9, Application US/09339912A

; Patent No. US20020099176A1

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven, M.

; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDG NR10

; TITLE OF INVENTION: (CCR5 Receptor)

; FILE REFERENCE: 1488.1150003

; CURRENT APPLICATION NUMBER: US/09/339,912A

; CURRENT FILING DATE: 1999-06-25

; PRIOR APPLICATION NUMBER: 09/195,662

; PRIOR FILING DATE: 1998-11-18

; PRIOR APPLICATION NUMBER: 08/466,343

; PRIOR FILING DATE: 1995-06-06

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9

; LENGTH: 329

; TYPE: PRT

; ORGANISM: Protein

US-09-339-912A-9

Query Match 87.7%; Score 1727.5; DB 9; Length 329;

Best Local Similarity 95.6%; Pred. No. 3.9e-142;

Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

```

Qy      18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
Db      1  EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60
Qy      78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
Db      61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105
Qy      138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
Db      106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

```

Qy	198	WNNFHTIMRNILGLVLPLLMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	257
Db	166	WNNFHTIMRNILGLVLPLLMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	225
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	317
Db	226	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	285
Qy	318	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKKSIG	361
Db	286	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKKSIG	329

Search completed: January 10, 2005, 11:57:29  
Job time : 752 secs

OM protein - protein search, using sw model

Run on: January 10, 2005, 11:27:37 ; Search time 193 Seconds  
(without alignments)  
1114.975 Million cell updates/sec

Title: US-10-791-592-2  
Perfect score: 1970  
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1970	100.0	374	1 CKR2_HUMAN	P41597 homo sapien
2	1614.5	82.0	360	1 CKR2_MACMU	O18793 macaca mula
3	1346.5	68.4	373	1 CKR2_RAT	O55193 rattus norv
4	1332.5	67.6	373	1 CKR2_MOUSE	P51683 mus musculu
5	1332.5	67.6	373	2 BAC32793	Bac32793 mus muscu
6	1327.5	67.4	373	2 Q6YT42	Q6yt42 sus scrofa
7	1327.5	67.4	373	2 BAD12134	Bad12134 sus scrof
8	1327.5	67.4	373	2 BAD08648	Bad08648 sus scrof
9	1327.5	67.4	373	2 BAD08655	Bad08655 sus scrof
10	1252	63.6	352	2 Q95NC2	Q95nc2 callicebus
11	1244	63.1	339	2 Q9TQT3	Q9tqt3 callithrix
12	1244	63.1	339	2 Q9TUV8	Q9tuv8 saguinus sp
13	1244	63.1	352	2 Q6WN98	Q6wn98 callithrix
14	1244	63.1	352	2 Q9MZA0	Q9mza0 callithrix
15	1244	63.1	352	2 AAQ20011	Aaq20011 callithri

16	1244	63.1	352	2	AAQ20012	Aaq20012 callithri
17	1244	63.1	352	2	AAQ20013	Aaq20013 callithri
18	1244	63.1	354	1	CKR5_MOUSE	P51682 mus musculu
19	1243	63.1	339	2	Q9TQV5	Q9tqv5 saguinus sp
20	1243	63.1	352	2	Q95NC4	Q95nc4 ateles geof
21	1241	63.0	352	2	Q6WN93	Q6wn93 leontopithe
22	1241	63.0	352	2	Q6WN96	Q6wn96 leontopithe
23	1241	63.0	352	2	Q6WN97	Q6wn97 cebuella py
24	1241	63.0	352	2	AAQ20014	Aaq20014 cebuella
25	1241	63.0	352	2	AAQ20015	Aaq20015 leontopit
26	1241	63.0	352	2	AAQ20018	Aaq20018 leontopit
27	1240	62.9	339	2	Q9TUW0	Q9tuw0 saguinus sp
28	1239	62.9	352	2	Q6YT41	Q6yt41 sus scrofa
29	1239	62.9	352	2	Q9MZ99	Q9mz99 ateles sp.
30	1239	62.9	352	2	BAD12135	Bad12135 sus scrof
31	1239	62.9	352	2	BAD08649	Bad08649 sus scrof
32	1239	62.9	352	2	BAD08656	Bad08656 sus scrof
33	1238.5	62.9	339	2	Q9TUV6	Q9tuv6 saguinus sp
34	1238	62.8	339	2	Q9TUW1	Q9tuw1 saguinus sp
35	1237	62.8	339	2	Q9TUV9	Q9tuv9 saguinus sp
36	1236	62.7	339	2	Q9TQW0	Q9tqw0 hylobates c
37	1236	62.7	352	1	CKR5_CERTO	O62743 cercocebus
38	1236	62.7	352	1	CKR5_HYLLE	O97883 hylobates l
39	1236	62.7	352	2	Q6WN92	Q6wn92 leontopithe
40	1236	62.7	352	2	Q6WN94	Q6wn94 leontopithe
41	1236	62.7	352	2	Q71RS2	Q71rs2 cercocebus
42	1236	62.7	352	2	Q8HZZ9	Q8hzt9 saimiri sci
43	1236	62.7	352	2	AAK69684	Aak69684 cercocebu
44	1236	62.7	352	2	AAQ20010	Aaq20010 saimiri s
45	1236	62.7	352	2	AAQ20017	Aaq20017 leontopit

# ALIGNMENTS

## RESULT 1

### CKR2\_HUMAN

ID CKR2\_HUMAN STANDARD; PRT; 374 AA.  
AC P41597;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)  
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).  
GN Name=CCR2; Synonyms=CMKBR2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94195821; PubMed=8146186;  
RA Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,  
RA Coughlin S.R.;  
RT "Molecular cloning and functional expression of two monocyte  
RT chemoattractant protein 1 receptors reveals alternative splicing of  
RT the carboxyl-terminal tails.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94324942; PubMed=8048929;  
 RA Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;  
 RT "cDNA cloning and functional expression of a human monocyte  
 RT chemoattractant protein 1 receptor."  
 RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97150864; PubMed=8995400;  
 RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;  
 RT "Organization and differential expression of the human monocyte  
 RT chemoattractant protein 1 receptor gene. Evidence for the role of the  
 RT carboxyl-terminal tail in receptor trafficking."  
 RL J. Biol. Chem. 272:1038-1045(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
 RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
 RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,  
 RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,  
 RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,  
 RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,  
 RA Sagripanti J.L.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.  
 RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,  
 RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;  
 RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-  
 RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [6]  
 RP SULFATION OF TYR-26, AND N-GLYCOSYLATION.  
 RX MEDLINE=20501139; PubMed=11046064;  
 RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,  
 RA Chakravarty L., Kolattukudy P.E.;  
 RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that  
 RT has tyrosine sulfation in a conserved extracellular N-terminal  
 RT region."  
 RL J. Immunol. 165:5295-5303(2000).  
 CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.  
 CC Transduces a signal by increasing the intracellular calcium ions  
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=A;  
 CC IsoId=P41597-1; Sequence=Displayed;  
 CC Name=B;  
 CC IsoId=P41597-2; Sequence=VSP\_001893;  
 CC -!- PTM: N-glycosylated.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----  
 DR EMBL; U03882; AAA19119.1; -.  
 DR EMBL; U03905; AAA19120.1; -.  
 DR EMBL; D29984; BAA06253.1; -.  
 DR EMBL; U80924; AAC51637.1; -.  
 DR EMBL; U80924; AAC51636.1; -.  
 DR EMBL; U95626; AAB57791.1; -.  
 DR EMBL; U95626; AAB57792.1; -.  
 DR EMBL; AF545480; AAN16400.1; -.  
 DR PIR; I38450; I38450.  
 DR PIR; JC2443; JC2443.  
 DR PDB; 1KAD; Model; A=1-349.  
 DR PDB; 1KP1; Model; A=1-349.  
 DR Genew; HGNC:1603; CCR2.  
 DR MIM; 601267; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005625; C:soluble fraction; TAS.  
 DR GO; GO:0004950; F:chemokine receptor activity; TAS.  
 DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .); TAS.  
 DR GO; GO:0006968; P:cellular defense response; TAS.  
 DR GO; GO:0006935; P:chemotaxis; TAS.  
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.  
 DR GO; GO:0006954; P:inflammatory response; TAS.  
 DR GO; GO:0007259; P:JAK-STAT cascade; TAS.  
 DR GO; GO:0007194; P:negative regulation of adenylate cyclase ac. . .; TAS.  
 DR InterPro; IPR002237; CC\_2\_receptor.  
 DR InterPro; IPR000355; Chm\_kine\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCR\_RHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW 3D-structure; Alternative splicing; G-protein coupled receptor;  
 KW Glycoprotein; Polymorphism; Sulfation; Transmembrane.  
 FT DOMAIN 1 42 Extracellular (Potential).  
 FT TRANSMEM 43 70 1 (Potential).  
 FT DOMAIN 71 80 Cytoplasmic (Potential).  
 FT TRANSMEM 81 100 2 (Potential).  
 FT DOMAIN 101 114 Extracellular (Potential).  
 FT TRANSMEM 115 136 3 (Potential).  
 FT DOMAIN 137 153 Cytoplasmic (Potential).  
 FT TRANSMEM 154 178 4 (Potential).  
 FT DOMAIN 179 206 Extracellular (Potential).  
 FT TRANSMEM 207 226 5 (Potential).  
 FT DOMAIN 227 243 Cytoplasmic (Potential).  
 FT TRANSMEM 244 268 6 (Potential).  
 FT DOMAIN 269 285 Extracellular (Potential).  
 FT TRANSMEM 286 309 7 (Potential).  
 FT DOMAIN 310 374 Cytoplasmic (Potential).  
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).  
 FT MOD\_RES 26 26 Sulfotyrosine.  
 FT DISULFID 113 190 By similarity.

FT VARSPLIC 314 374 SLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGR  
 FT GKKGKSIGRAPEASLQDKEGA -> RYLSVFFRKHITKRFEK  
 FT QCPVFYRETVDGVTSTNTPSTGEQEVSAAGL (in  
 FT isoform B).  
 FT /FTId=VSP\_001893.  
 FT VARIANT 64 64 V -> I (in dbSNP:1799864).  
 FT /FTId=VAR\_014339.  
 FT VARIANT 355 355 G -> E.  
 FT /FTId=VAR\_014340.  
 SQ SEQUENCE 374 AA; 41914 MW; F865E0D39E74CF0F CRC64;

Query Match 100.0%; Score 1970; DB 1; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-120;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy 361 GRAPEASLQDKEGA 374  
 ||||||||||||||||  
 Db 361 GRAPEASLQDKEGA 374

# RESULT 2

## CKR2\_MACMU

ID CKR2\_MACMU STANDARD; PRT; 360 AA.  
 AC O18793;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR2)  
 DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).  
 GN Name=CCR2; Synonyms=CMKBR2;  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21354176; PubMed=11461684; DOI=10.1089/088922201750290104;  
 RA Margulies B.J., Hauer D.A., Clements J.E.;  
 RT "Identification and comparison of eleven rhesus macaque chemokine  
 RT receptors.";  
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).  
 CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.  
 CC Transduces a signal by increasing the intracellular calcium ions  
 CC level.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=B;  
 CC IsoId=O18793-1; Sequence=Displayed;  
 CC Name=A;  
 CC IsoId=O18793-2; Sequence=Not described;  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF013958; AAD11572.1; -.  
 DR InterPro; IPR002237; CC\_2\_receptor.  
 DR InterPro; IPR000355; Chmkine\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Alternative splicing; G-protein coupled receptor; Glycoprotein;  
 KW Sulfation; Transmembrane.  
 FT DOMAIN 1 42 Extracellular (Potential).  
 FT TRANSMEM 43 70 1 (Potential).  
 FT DOMAIN 71 80 Cytoplasmic (Potential).  
 FT TRANSMEM 81 100 2 (Potential).  
 FT DOMAIN 101 114 Extracellular (Potential).  
 FT TRANSMEM 115 136 3 (Potential).  
 FT DOMAIN 137 153 Cytoplasmic (Potential).  
 FT TRANSMEM 154 178 4 (Potential).  
 FT DOMAIN 179 206 Extracellular (Potential).  
 FT TRANSMEM 207 226 5 (Potential).  
 FT DOMAIN 227 243 Cytoplasmic (Potential).  
 FT TRANSMEM 244 268 6 (Potential).  
 FT DOMAIN 269 285 Extracellular (Potential).  
 FT TRANSMEM 286 309 7 (Potential).  
 FT DOMAIN 310 360 Cytoplasmic (Potential).  
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).  
 FT MOD\_RES 26 26 Sulfotyrosine (By similarity).  
 FT DISULFID 113 190 By similarity.



SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;

Query Match 82.0%; Score 1614.5; DB 1; Length 360;  
Best Local Similarity 96.6%; Pred. No. 2.4e-97;  
Matches 308; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      |||
Db      1 MLSTSRSRFIRNTNGSGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
      |||
Db     61 MLVVLILINCKKLKSLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      |||
Db    121 HIGYLGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
      ||:|||||
Db    181 CQEEDSVYICGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      |||:|||||
Db    241 AVRLIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTRQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFR---SLF 316
      |||
Db    301 NPIIYAFVGEKFRRYLSMF 319
```

RESULT 3

CKR2\_RAT

ID CKR2\_RAT STANDARD; PRT; 373 AA.  
AC O55193;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2).  
GN Name=Ccr2; Synonyms=Cmkbr2;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=98318173; PubMed=9655467;  
RA Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,  
RA deFiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;  
RT "Chemokine receptor expression in cultured glia and rat experimental  
RT allergic encephalomyelitis.";  
RL J. Neuroimmunol. 86:1-12(1998).  
CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5  
CC chemokines. Transduces a signal by increasing the intracellular  
CC calcium ions level (By similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.



Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLMVICYSGILKTLRLCRNEKKRHR 240  
 Db 194 SEQEDDQHTCGPYFPTIWKNFQTIMRNILSLILPLLMVICYSGILHTLFRRCRNEKKRHR 253

Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300  
 Db 254 AVRLIFAIMIVYFLFWTPYNIVLFLTTFQEFLGMSNCVVDMLDQAMQVTETLGMTHCCV 313

Qy 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327  
 Db 314 NPIIYAFVGEKFRRLYSIFFRKHIAKNLCKQCPV 347

#### RESULT 4

##### CKR2\_MOUSE

ID CKR2\_MOUSE STANDARD; PRT; 373 AA.  
 AC P51683; Q61172;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)  
 DE (JE/FIC receptor) (MCP-1 receptor).  
 GN Name=Ccr2; Synonyms=Cmkbr2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96205938; PubMed=8631787;  
 RA Boring L., Gosling J., Montecarlo F.S., Lusic A.J., Tsou C.-L.,  
 RA Charo I.F.;  
 RT "Molecular cloning and functional expression of murine JE (monocyte  
 RT chemoattractant protein 1) and murine macrophage inflammatory protein  
 RT 1alpha receptors: evidence for two closely linked C-C chemokine  
 RT receptors on chromosome 9.";  
 RL J. Biol. Chem. 271:7551-7558(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=96216064; PubMed=8662823;  
 RA Kurihara T., Bravo R.;  
 RT "Cloning and functional expression of mCCR2, a murine receptor for the  
 RT C-C chemokines JE and FIC.";  
 RL J. Biol. Chem. 271:11603-11606(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97026720; PubMed=8872898;  
 RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,  
 RA Post T.W., Gerard C., Dorf M.E.;  
 RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse  
 RT transcriptase-polymerase chain reaction does not detect mRNA for the  
 RT KC or new MCP-1 receptor.";  
 RL J. Neurosci. Res. 45:382-391(1996).  
 CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5  
 CC chemokines. Transduces a signal by increasing the intracellular

CC calcium ions level.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,  
 CC but not in nonhematopoietic cell lines.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U47035; AAC52453.1; -.  
 DR EMBL; U51717; AAC52557.1; -.  
 DR EMBL; U56819; AAC52784.1; -.  
 DR MGD; MGI:106185; Ccr2.  
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.  
 DR GO; GO:0019955; F:cytokine binding; IPI.  
 DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.  
 DR GO; GO:0030097; P:hemopoiesis; IMP.  
 DR GO; GO:0006959; P:humoral immune response; IMP.  
 DR GO; GO:0006954; P:inflammatory response; IMP.  
 DR GO; GO:0019233; P:perception of pain; IMP.  
 DR GO; GO:0030334; P:regulation of cell migration; IMP.  
 DR InterPro; IPR002237; CC\_2\_receptor.  
 DR InterPro; IPR000355; Chmkine\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane.  
 FT DOMAIN 1 55 Extracellular (Potential).  
 FT TRANSMEM 56 83 1 (Potential).  
 FT DOMAIN 84 93 Cytoplasmic (Potential).  
 FT TRANSMEM 94 114 2 (Potential).  
 FT DOMAIN 115 127 Extracellular (Potential).  
 FT TRANSMEM 128 149 3 (Potential).  
 FT DOMAIN 150 166 Cytoplasmic (Potential).  
 FT TRANSMEM 167 191 4 (Potential).  
 FT DOMAIN 192 219 Extracellular (Potential).  
 FT TRANSMEM 220 239 5 (Potential).  
 FT DOMAIN 240 256 Cytoplasmic (Potential).  
 FT TRANSMEM 257 281 6 (Potential).  
 FT DOMAIN 282 298 Extracellular (Potential).  
 FT TRANSMEM 299 322 7 (Potential).  
 FT DOMAIN 323 373 Cytoplasmic (Potential).  
 FT DISULFID 126 203 By similarity.  
 FT CONFLICT 39 39 Y -> H (in Ref. 1).  
 FT CONFLICT 184 184 A -> G (in Ref. 1).  
 FT CONFLICT 264 264 V -> G (in Ref. 1).  
 SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 67.6%; Score 1332.5; DB 1; Length 373;  
 Best Local Similarity 76.3%; Pred. No. 5.5e-79;

Matches 255; Conservative 26; Mismatches 46; Indels 7; Gaps 3;

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      :||| | | | : | | | | :|| | ||| ||||| :|||||||
Db      14 ILSTSHSLFTRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN 73

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
      |||::||| ||||| :|||||||:||| ||| ||||| |||:|||||
Db     74 MLVIIILIGCKKLKSMTDIYLLNLAISDLLFLLLTLPFWAHYAANEWVFGNIMCKVFTGLY 133

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      |||||:|||||:|||||:|||||:|||||:|||||
Db    134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVITSVVTWVAVFASLPGIIFTK 193

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRCRNEKKRHR 240
      ::| | |||| : | | ||||| :|||:||||| || |||||
Db    194 SKQDDHHYTCGPYFTQLWKNFQTIMRNILSLILPLLMVICYSGILHTLFRCRNEKKRHR 253

Qy    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      |||:| | |||||:| ||| |:|| | ||| |||||
Db    254 AVRLIFAIMIVYFLFWTPYNIVLFLTTFQESLGMSNCVIDKHLDDQAMQVTETLGMTHCCI 313

Qy    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
      ||:||||||| |:|| ||| |: |:
Db    314 NPVIYAFVGEKFRRYLSIFFRKHIKRLCKQCPV 347

```

# RESULT 5

BAC32793

```

ID   BAC32793     PRELIMINARY;          PRT;   373 AA.
AC   BAC32793;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   4 days neonate male adipose cDNA, RIKEN full-length enriched library,
DE   clone:B430108F19 product:chemokine (C-C) receptor 2, full insert
DE   sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Adipose;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Adipose;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).

```

RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Adipose;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Adipose;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Adipose;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Adipose;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AK046579; BAC32793.1; -.  
 KW Receptor.  
 SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 67.6%; Score 1332.5; DB 2; Length 373;  
 Best Local Similarity 76.3%; Pred. No. 5.5e-79;  
 Matches 255; Conservative 26; Mismatches 46; Indels 7; Gaps 3;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60  
 :||||| | | : | | || :||| | |||| ||||| :|||||||  
 Db 14 ILSTSHSLFTRSIQELDEGATTPYDYGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN 73

Qy 61 MLVVLILINCKKCLKLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120  
 |||::||| ||||| :|||||||:|||| ||| ||||| |||:|||||  
 Db 74 MLVILIGCKKLSMTDIYLLNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKVFTGLY 133

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVITSVVTWVAVFASLPGIIFTK 193

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240  
 ::| | |||| : | | ||||| |:||||:||||||| | | |||||  
 Db 194 SKQDDHHYTCGPYFTQLWKNFQTIMRNILSLILPLVMVICYSGILHTLFRNEKKRHR 253

Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300  
 |||:| | |||||:| |||| |:| | ||| |||||  
 Db 254 AVRLIFAIMIVYFLFWTPYNIVLFLTTFQESLGMSNCVIDKHLDQAMQVTETLGMTHCCI 313

Qy 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327  
 ||:||||||| | :| ||| |: | :  
 Db 314 NPVIYAFVGEKFRRYLSIFFRKHIARLCKQCPV 347

# RESULT 6

Q6YT42

ID Q6YT42 PRELIMINARY; PRT; 373 AA.  
 AC Q6YT42;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Chemokine (C-C motif) receptor 2 (Chemokine C-C motif receptor  
 DE 2).  
 GN Name=CCR2;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,  
 RA Uenishi H.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AP006185; BAD08648.1; -.  
 DR EMBL; AP006435; BAD08655.1; -.  
 DR EMBL; AB119271; BAD12134.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR002237; CC\_2\_receptor.  
 DR InterPro; IPR000355; Chmkine\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00657; CCHEMOKINER.

DR PRINTS; PR01107; CHEMOKINER2.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 373 AA; 42299 MW; FA8E55CA527A34E0 CRC64;

Query Match 67.4%; Score 1327.5; DB 2; Length 373;  
 Best Local Similarity 76.0%; Pred. No. 1.2e-78;  
 Matches 254; Conservative 29; Mismatches 44; Indels 7; Gaps 3;

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          :| || |   | : || || :||| || | | | | |||||
Db      14 VLPTSHSLLTMNIKGNDEEPTTSYDYDYSEPCQKTSVGQIEALLPPLYSLVFIFGFVGN 73

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
          :||| ||||| :||| ||||| ||:| || ||: ||| || ||||
Db     74 LLVVLILINCKKLKSMTDIYLLNLAISDLLFLFTIPFWAHYAADQWVFGNIMCKFFTGLY 133

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          ||||| ||||| ||||| ||||| ||||| ||||| :||: ||: ||: ||| :
Db    134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAIFASLPGIIFIR 193

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240
          |:| | | | ||| | |||||: |||||: ||: ||||| ||||| |:| :
Db    194 SQEEHSGYACAPYFPLAWKNFHTIMRSILGLVLP LLVMVVCYSGILKTL LRCRNEKKKHK 253

Qy    241 AVRVI FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
          |||: || ||||| ||||: ||: || |||||: ||: ||||| |||||: ||||
Db    254 AVRLIFVIMIVYFLFWAPYNIVLLLSTFQVFFGLSNCKNSSQLDQAMQVTETLGLTHCCI 313

Qy    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
          ||||| ||||| |:| ||| |:| :
Db    314 NPIIYAFVGEKFRRYLSVFFRKHI AKHLCKQCPV 347
  
```

# RESULT 7

BAD12134

ID BAD12134 PRELIMINARY; PRT; 373 AA.  
 AC BAD12134;  
 DT 03-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 03-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 03-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Chemokine C-C motif receptor 2.  
 GN CCR2.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,  
 RA Uenishi H.;  
 RT "Analysis of genomic structure of porcine CC chemokine receptor genes  
 RT and their expression."  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB119271; BAD12134.1; -.



KW Receptor.

SQ SEQUENCE 373 AA; 42299 MW; FA8E55CA527A34E0 CRC64;

Query Match 67.4%; Score 1327.5; DB 2; Length 373;

Best Local Similarity 76.0%; Pred. No. 1.2e-78;

Matches 254; Conservative 29; Mismatches 44; Indels 7; Gaps 3;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      :| || |   |   : || || :||| || | | || | ||||| |||||
Db      14 VLPTSHSLLTMNIKGNDEEPTTSYDYDYSEPCQKTSVGQIEALLPPLYSLVFIFGFVGN 73

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
      :||| ||||| ||| :||| ||||| ||| :| || | ||: ||| || ||||
Db     74 LLVVLILINCKKLKSMTDIYLLNLAISDLLFLFTIPFWAHYAADQWVFGNIMCKFFTGLY 133

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :||: ||: |||| :
Db    134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFIR 193

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240
      |:| | | | ||| | ||||| :||| ||||| :||: ||||| ||||| ||||| :|:
Db    194 SQEEHSGYACAPYFPLAWKNFHTIMRSILGLVLP LLVMVVCYSGILKTL LRCRNEKKKHK 253

Qy    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      |||: || ||||| ||||| :||: ||| ||||| :||: ||||| ||||| :|||
Db    254 AVRLIFVIMIVYFLFWAPYNIVLLSTFQVFFGLSNCKNSSQLDQAMQVTETLGLTHCCI 313

Qy    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
      ||||| ||||| | :| ||| | : | :
Db    314 NPIIYAFVGEKFRRYLSVFFRKHIAKHLCKQCPV 347
```

#### RESULT 8

BAD08648

ID BAD08648 PRELIMINARY; PRT; 373 AA.

AC BAD08648;

DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE Chemokine (C-C motif) receptor 2.

GN CCR2.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;

RT "Cloning of porcine CC chemokine receptor genes and clustering

RT structure on SSC13.";

RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AP006185; BAD08648.1; -.

KW Receptor.

SQ SEQUENCE 373 AA; 42299 MW; FA8E55CA527A34E0 CRC64;

Query Match 67.4%; Score 1327.5; DB 2; Length 373;

Best Local Similarity 76.0%; Pred. No. 1.2e-78;

Matches 254; Conservative 29; Mismatches 44; Indels 7; Gaps 3;

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      :| || |   |   : || || :||| || | | || | |||||
Db      14 VLPTSHSLLTMNIKGNDEEPTTSYDYDYSEPCQKTSVGQIEALLPPLYSLVFIFGFVGN 73

Qy      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
      :||| ||||| :||| ||||| ||:| || | ||: |||| || | ||||
Db      74 LLVVLILINCKKLKSMTDIYLLNLAISDLLFLFTIPFWAHYAADQWVFGNIMCKFFTGLY 133

Qy     121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      ||||| ||||| ||||| ||||| ||||| :||: ||: ||: |||| :
Db     134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAIFASLPGIIFIR 193

Qy     181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
      |:| | | | ||| | |||||: |||||: ||: ||||| |||||: |:
Db     194 SQEEHSGYACAPYFPLAWKNFHTIMRSILGLVLP LLVMVVCYSGILKTLLRCRNEKKKHK 253

Qy     241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      |||: || ||||| ||||: ||: || |||||: ||: ||||| |||||: ||||
Db     254 AVRLIFVIMIVYFLFWAPYNIVLLLSTFQVFFGLSNCKNSSQLDQAMQVTETLGLTHCCI 313

Qy     301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
      ||||| ||||| |:| ||| |: |:
Db     314 NPIIYAFVGEKFRRYLSVFFRKHIAKHLCKQCPV 347

```

# RESULT 9

BAD08655

```

ID   BAD08655    PRELIMINARY;          PRT;   373 AA.
AC   BAD08655;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Chemokine (C-C motif) receptor 2.
GN   CCR2.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RT   "Cloning of porcine CC chemokine receptor genes and clustering
RT   structure on SSC13.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP006435; BAD08655.1; -.
KW   Receptor.
SQ   SEQUENCE   373 AA;  42299 MW;  FA8E55CA527A34E0 CRC64;

```

Query Match 67.4%; Score 1327.5; DB 2; Length 373;  
 Best Local Similarity 76.0%; Pred. No. 1.2e-78;  
 Matches 254; Conservative 29; Mismatches 44; Indels 7; Gaps 3;

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      :| || |   |   : || || :||| || | | || | |||||
Db      14 VLPTSHSLLTMNIKGNDEEPTTSYDYDYSEPCQKTSVGQIEALLPPLYSLVFIFGFVGN 73

```



DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;

Query Match 63.6%; Score 1252; DB 2; Length 352;  
 Best Local Similarity 76.1%; Pred. No. 9e-74;  
 Matches 239; Conservative 26; Mismatches 37; Indels 12; Gaps 3;

Qy 18 EEVTTFFDYDYGA--PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKC 75  
 | : :| ||| || | |||:|||||||:|:|||||||:|  
 Db 4 EVSSPIYDIDYGASEPCQKIDVKQMGAGQLLPPLYSMVFLFGFVGNMLVVLILINCKRLKS 63

Qy 76 LTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLT 135  
 :||||||| || |:| ||| || :| ||| ||: ||| ||:| |||||  
 Db 64 MTDIYLLNLAISDLFFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIIFIILLT 123

Qy 136 IDRYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTKQKEDSVYVCGPYFP 195  
 |||||||:|||||:|||||:|||||: ||| | | |:|  
 Db 124 IDRYLAIVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGYHYTCSPHFP 183

Qy 196 RG----WNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHRVRIFTIMIV 251  
 | | | |: |||||:|||||:|||||:|||||  
 Db 184 FGQYRFWKNLETLMVILGLVLPLLMVICYSGILKTLRLCRNEKKRHRVRLIFTIMIV 243

Qy 252 YFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEK 311  
 ||||| ||||:||||:||||:| | |:| ||| |||||:|||||  
 Db 244 YFLFWAPYNIVLLNTYQEFFGLNNCSSNRDQAMQVTETLGMTHCCVNPIIYAFVGEK 303

Qy 312 FRSLF-----HIA 319  
 ||: |||  
 Db 304 FRNYLLVFFQKHIA 317

# RESULT 11

## Q9TQT3

ID Q9TQT3 PRELIMINARY; PRT; 339 AA.  
 AC Q9TQT3;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN Name=CCR5;  
 OS Callithrix jacchus (Common marmoset).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.  
 OX NCBI\_TaxID=9483;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22942991; PubMed=14581567;  
 RA Kunstman K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R.,  
 RA Kunstman J., Stanton J., Agy M., Shibata R., Yoder A.D., Pillai S.,  
 RA Doms R.W., Marx P., Wolinsky S.M.;  
 RT "Structure and function of CC-chemokine receptor 5 homologues derived  
 RT from representative primate species and subspecies of the taxonomic  
 RT suborders Prosimii and Anthropoidea.";  
 RL J. Virol. 77:12310-12318(2003).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AF162021; AAD47776.1; -.  
 DR EMBL; AF161934; AAD47691.1; -.  
 DR EMBL; AF161935; AAD47692.1; -.  
 DR EMBL; AF161936; AAD47693.1; -.  
 DR EMBL; AF161937; AAD47694.1; -.  
 DR EMBL; AF161938; AAD47695.1; -.  
 DR EMBL; AF161939; AAD47696.1; -.  
 DR EMBL; AF161940; AAD47697.1; -.  
 DR EMBL; AF161944; AAD47700.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000923; BlueCu\_1.  
 DR InterPro; IPR002240; CC\_5\_receptor.  
 DR InterPro; IPR000355; Chmkine\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00657; CCHEMOKINER.  
 DR PRINTS; PR01110; CHEMOKINER5.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00196; COPPER\_BLUE; UNKNOWN\_1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39055 MW; C1313952E71B50C7 CRC64;

Query Match 63.1%; Score 1244; DB 2; Length 339;  
 Best Local Similarity 76.6%; Pred. No. 2.9e-73;  
 Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;

Qy 24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81  
 :| ||| || | ||||:| |||||:|:|||||:|:|||||  
 Db 3 YDIDYGPSEPCRKIDVKQMGALLPPLYSMVFLFGFVGNMLVVLILINCKRLKSMTDIYL 62  
  
 Qy 82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141  
 |||||:| |:| ||| || |:| ||| ||: ||| |:| |||||  
 Db 63 LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA 122  
  
 Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197  
 |||||:|:|||||:|||||: ||| | |:| :  
 Db 123 IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGYHYTCSPHPFQSQYQF 182  
  
 Qy 198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 257  
 | || |: |||||:|||||:|||||:|:|||||  
 Db 183 WKNFETLKMVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWA 242

Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316  
 |||||:||||:|||||:| |::||| |||||:|||||:|||||:  
 Db 243 PYNIVLLLNTYQEFFGLNNCSSNRDLQAMQVTETLGMTHCCVNPPIIYAFVGEKFRNYLA 302  
 Qy 317 -----HIA 319  
 |||  
 Db 303 VFFQKHIA 310

RESULT 12

Q9TUV8

ID Q9TUV8 PRELIMINARY; PRT; 339 AA.  
 AC Q9TUV8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN Name=CCR5;  
 OS Saguinus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.  
 OX NCBI\_TaxID=100754;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22942991; PubMed=14581567;  
 RA Kunstman K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R.,  
 RA Kunstman J., Stanton J., Agy M., Shibata R., Yoder A.D., Pillai S.,  
 RA Doms R.W., Marx P., Wolinsky S.M.;  
 RT "Structure and function of CC-chemokine receptor 5 homologues derived  
 RT from representative primate species and subspecies of the taxonomic  
 RT suborders Prosimii and Anthropoidea.";  
 RL J. Virol. 77:12310-12318(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AF161929; AAD47686.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000923; BlueCu\_1...  
 DR InterPro; IPR002240; CC\_5\_receptor.  
 DR InterPro; IPR000355; Chmkine\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00657; CCHEMOKINER.  
 DR PRINTS; PR01110; CHEMOKINER5.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00196; COPPER\_BLUE; UNKNOWN\_1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.

FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39164 MW; 6A67CF5D22C70C49 CRC64;

Query Match 63.1%; Score 1244; DB 2; Length 339;  
 Best Local Similarity 77.3%; Pred. No. 2.9e-73;  
 Matches 238; Conservative 24; Mismatches 34; Indels 12; Gaps 3;

Qy 24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81  
 :| ||| || | ||||:| | |||||:|:| ||||| |||||: | :|||  
 Db 3 YDIDYGPSEPCRKIDVKQMGHLLPPLYSMVFLFGFVGNMLVVLILINCKRPKSMTDIYL 62

Qy 82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTIDRYLA 141  
 |||||:| | :| ||| || :| ||| ||: ||| ||:| ||||| |||||  
 Db 63 LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIIFFIILLTIDRYLA 122

Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---- 197  
 |||||:| | :| ||| ||: ||| ||: ||| ||:| ||||| |||||  
 Db 123 IVHAVFALKARTVTFGVVTSVITWLVAVFASLPGIIFTRSQKEGYHYTCSPHYFPGQYQF 182

Qy 198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRIFTIMIVYFLFWT 257  
 | || |: ||||| ||||| ||||| |||||: ||||| |||||  
 Db 183 WKNFETLKMVILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRLIFTIMIVYFLFWA 242

Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316  
 ||||:| | :| ||||:| | :| ||| ||||| ||||| |||||:|  
 Db 243 PYNIVLLLNTYQEFFGLNCSNRDLQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLV 302

Qy 317 -----HIA 319  
 |||  
 Db 303 VFFQKHIA 310

# RESULT 13

Q6WN98

ID Q6WN98 PRELIMINARY; PRT; 352 AA.  
 AC Q6WN98;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE CC chemokine receptor 5.  
 GN Name=ccr5;  
 OS Callithrix humeralifera (tassel-eared marmoset).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.  
 OX NCBI\_TaxID=52232;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,  
 RA Seuanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AY278745; AAQ20013.1; -.  
 DR EMBL; AY278744; AAQ20012.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR000923; BlueCu\_1.

DR InterPro; IPR002240; CC\_5\_receptor.  
 DR InterPro; IPR000355; Chmkine\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00657; CCHEMOKINER.  
 DR PRINTS; PR01110; CHEMOKINER5.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00196; COPPER\_BLUE; UNKNOWN\_1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 352 AA; 40522 MW; FF0D0A852E553AF5 CRC64;

Query Match 63.1%; Score 1244; DB 2; Length 352;  
 Best Local Similarity 76.6%; Pred. No. 3e-73;  
 Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;

Qy	24	FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL	81
		:               :       : :             :	
Db	10	YDIDYGPSEPCRKIDVKQGAHLLPPLYSMVFLFGFVGNMLVVLILINCKRLKSMTDIYL	69
Qy	82	LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA	141
		:     :          :        :       :	
Db	70	LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA	129
Qy	142	IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG	197
		:      :      :          :    :	
Db	130	IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGYHYTCSPHFPFSQYQF	189
Qy	198	WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT	257
		:      :            :	
Db	190	WKNFETLKMVILGLVLPLLMVICYSGILKTLLRCRNEKKRHRRAVRLIFTIMIVYFLFWA	249
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF-	316
		:      :      :      :                 :      :	
Db	250	PYNIVLLLNTYQEFFGLNCSNRDLQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLK	309
Qy	317	-----HIA	319
Db	310	VFFQKHIA	317

# RESULT 14

Q9MZA0

ID Q9MZA0 PRELIMINARY; PRT; 352 AA.  
 AC Q9MZA0;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE CC chemokine receptor 5 (Chemokine receptor CCR5).  
 GN Name=CCR5; Synonyms=ccr5;  
 OS Callithrix jacchus (Common marmoset).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.  
 OX NCBI\_TaxID=9483;  
 RN [1]  
 RP SEQUENCE FROM N.A.







[illegible]

Search completed: January 10, 2005, 11:33:39  
Job time : 195 secs